

10/500796 #6

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SEQUENCE LISTING

<110> The Government of the United States of America, as represented by the Secretary, Department of Health and Human Services, Centers for Disease Control and Prevention

Chang, Gwong-Jen J

<120> Nucleic Acid Vaccines for Prevention of Flavivirus Infection

<130> 6395-64909-02

<150> PCT/US02/10764

<151> 2002-04-04

<150> 09/826,115

<151> 2001-04-04

<150> 09/701,536

<151> 2000-11-29

<150> PCT/US99/12298

<151> 1999-06-03

<150> 60/087,908

<151> 1998-06-04

<160> 61

<170> FastSEQ for Windows Version 4.0

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<222> (25)...(48)

<221> misc_feature

<222> 1-48

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cat ggg aat tat tca gcg caa gtt ggg gcg tcc cag gcg gca aag ttt His Gly Asn Tyr Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe 350 355 360	2007
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synthetic construct

<223> pCDJE 2-7

<400> 11

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Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu Gly Ser Ile Met
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Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Met Lys
          20          25          30
Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile Asn Asn Thr Asp
          35          40          45
Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly Glu Asn Arg Cys
          50          55          60
Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu Asp Thr Ile Thr
          65          70          75          80
Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro Glu Asp Val Asp
          85          90          95
Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr Gly Arg Cys Thr
          100         105         110
Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val Ser Val Gln Thr
          115         120         125
His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala Trp Leu Asp Ser
          130         135         140
Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn Trp Ile Ile Arg
          145         150         155         160
Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly Trp Met Leu Gly
          165         170         175
Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu Leu Leu Leu Val
          180         185         190
Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly Asn Arg Asp Phe
          195         200         205
Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly

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210	215	220
Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro Thr Leu Asp Val		
225	230	235
Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu Val Arg Ser Tyr		
	245	250
Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val Ala Arg Cys Pro		
	260	265
Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp Ser Ser Tyr Val		
	275	280
Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu		
	290	295
Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe Ser Cys Thr Ser		
305	310	315
Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile Lys Tyr Glu Val		
	325	330
Gly Ile Phe Val His Gly Thr Thr Thr Ser Glu Asn His Gly Asn Tyr		
	340	345
Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe Thr Val Thr Pro		
	355	360
Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr Gly Glu Val Thr		
	370	375
Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu Ala Phe Tyr Val		
385	390	395
Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg Glu Trp Phe His		
	405	410
Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr Ala Trp Arg Asn		
	420	425
Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala Thr Lys Gln Ser		
	435	440
Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His Gln Ala Leu Ala		
	450	455
Gly Ala Ile Val Val Glu Tyr Ser Ser Ser Val Lys Leu Thr Ser Gly		
465	470	475
His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala Leu Lys Gly Thr		
	485	490
Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala Lys Asn Pro Ala		
	500	505
Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser Tyr Ser Gly Ser		
	515	520
		525

Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala Ser Leu Asn Asp		
530	535	540
Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ala Thr		
545	550	555
Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu Pro Pro Phe Gly		
	565	570
Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln Ile Asn His His		
	580	585
Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe Ser Thr Thr Leu		
	595	600
Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe		
	610	615
Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln		
625	630	635
Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile		
	645	650
		655

Thr	Gln	Gly	Leu	Met	Gly	Ala	Leu	Leu	Leu	Trp	Met	Gly	Val	Asn	Ala
			660					665					670		
Arg	Asp	Arg	Ser	Ile	Ala	Leu	Ala	Phe	Leu	Ala	Thr	Gly	Gly	Val	Leu
		675					680					685			
Val	Phe	Leu	Ala	Thr	Asn	Val	His	Ala							
	690					695									

<210> 12
 <211> 46
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note =
 synthetic construct

<221> misc_feature
 <222> 1-46
 <223> WN 466

<400> 12
 cttggtaccc gtctcggcgc cgtgaccctc tcgaacttcc agggca 46

<210> 13
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note =
 synthetic construct

<221> misc_feature
 <222> 1-43
 <223> CWN2444

<400> 13
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<210> 14
 <211> 24
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note =
 synthetic construct

<223> JE Signal

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Val	Val	Ile	Ala	Cys	Ala	Gly	Ala								
			20												

<210> 15

<211> 5308
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
 synthetic construct

<221> CDS

<222> (911)...(2987)

<221> misc_feature

<222> (1)...(5308)

<223> pCBWN

<400> 15

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ccgcatagtt	aagccagtat	ctgctccctg	cttgtgtgtt	ggaggtcgct	gagtagtgcg	120
cgagcaaaat	ttaagctaca	acaaggcaag	gcttgaccga	caattgcatg	aagaatctgc	180
ttagggtag	gcgttttgcg	ctgcttcgcg	atgtacgggc	cagatatacg	cgttgacatt	240
gattattgac	tagttattaa	tagtaatcaa	ttacggggtc	attagttcat	agcccatata	300
tggagttccg	cgttacataa	cttacggtaa	atggcccgcg	tggctgaccg	cccaacgacc	360
cccgccatt	gacgtcaata	atgacgtatg	ttcccatagt	aacgcccaata	gggactttcc	420
attgacgtca	atgggtggag	tatttacggg	aaactgccc	cttggcagta	catcaagtgt	480
atcatatgcc	aagtacgccc	cctattgacg	tcaatgacgg	taaatggccc	gcctggcatt	540
atgcccagta	catgacctta	tgggactttc	ctacttggca	gtacatctac	gtattagtca	600
tcgctattac	catggtgatg	cggtttttgg	cagtacatca	atgggcgtgg	atagcggttt	660
gactcacggg	gatttccaag	tctccacccc	attgacgtca	atgggagttt	gttttggcac	720
caaaatcaac	gggactttcc	aaaatgtcgt	aacaactccg	ccccattgac	gcaaattgggc	780
ggtaggcgtg	tacggtggga	ggtctatata	agcagagctc	tctggctaac	tagagaaccc	840
actgcttact	ggcttatcga	aattaatacg	actcactata	gggagaccca	agcttggtac	900
cgccgccgcc	atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg					949
	Met Gly Lys Arg Ser Ala Gly Ser	Ile Met Trp Leu Ala				
	1	5	10			

agc ttg gca gtt gtc ata gct tgt gca ggc gcc	gtg acc ctc tcg aac	997
Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala	Val Thr Leu Ser Asn	
15	20	25

ttc cag ggc aag gtg atg atg acg gta aat gct act gac gtc aca gat	1045		
Phe Gln Gly Lys Val Met Met Thr Val Asn Ala Thr Asp Val Thr Asp			
30	35	40	45

gtc atc acg att cca aca gct gct gga aag aac cta tgc att gtc aga	1093	
Val Ile Thr Ile Pro Thr Ala Ala Gly Lys Asn Leu Cys Ile Val Arg		
50	55	60

gca atg gat gtg gga tac atg tgc gat gat act atc act tat gaa tgc	1141	
Ala Met Asp Val Gly Tyr Met Cys Asp Asp Thr Ile Thr Tyr Glu Cys		
65	70	75

cca gtg ctg tcg gct ggt aat gat cca gaa gac atc gac tgt tgg tgc	1189	
Pro Val Leu Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys		
80	85	90

aca aag tca gca gtc tac gtc agg tat gga aga tgc acc aag aca cgc	1237
Thr Lys Ser Ala Val Tyr Val Arg Tyr Gly Arg Cys Thr Lys Thr Arg	
95 100 105	
cac tca aga cgc agt cgg agg tca ctg aca gtg cag aca cac gga gaa	1285
His Ser Arg Arg Ser Arg Ser Leu Thr Val Gln Thr His Gly Glu	
110 115 120 125	
agc act cta gcg aac aag aag ggg gct tgg atg gac agc acc aag gcc	1333
Ser Thr Leu Ala Asn Lys Lys Gly Ala Trp Met Asp Ser Thr Lys Ala	
130 135 140	
aca agg tat ttg gta aaa aca gaa tca tgg atc ttg agg aac cct gga	1381
Thr Arg Tyr Leu Val Lys Thr Glu Ser Trp Ile Leu Arg Asn Pro Gly	
145 150 155	
tat gcc ctg gtg gca gcc gtc att ggt tgg atg ctt ggg agc aac acc	1429
Tyr Ala Leu Val Ala Ala Val Ile Gly Trp Met Leu Gly Ser Asn Thr	
160 165 170	
atg cag aga gtt gtg ttt gtc gtg cta ttg ctt ttg gtg gcc cca gct	1477
Met Gln Arg Val Val Phe Val Val Leu Leu Leu Leu Val Ala Pro Ala	
175 180 185	
tac agc ttc aac tgc ctt gga atg agc aac aga gac ttc ttg gaa gga	1525
Tyr Ser Phe Asn Cys Leu Gly Met Ser Asn Arg Asp Phe Leu Glu Gly	
190 195 200 205	
gtg tct gga gca aca tgg gtg gat ttg gtt ctc gaa ggc gac agc tgc	1573
Val Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys	
210 215 220	
gtg act atc atg tct aag gac aag cct acc atc gat gtg aag atg atg	1621
Val Thr Ile Met Ser Lys Asp Lys Pro Thr Ile Asp Val Lys Met Met	
225 230 235	
aat atg gag gcg gcc aac ctg gca gag gtc cgc agt tat tgc tat ttg	1669
Asn Met Glu Ala Ala Asn Leu Ala Glu Val Arg Ser Tyr Cys Tyr Leu	
240 245 250	
gct acc gtc agc gat ctc tcc acc aaa gct gcg tgc ccg acc atg gga	1717
Ala Thr Val Ser Asp Leu Ser Thr Lys Ala Ala Cys Pro Thr Met Gly	
255 260 265	
gaa gct cac aat gac aaa cgt gct gac cca gct ttt gtg tgc aga caa	1765
Glu Ala His Asn Asp Lys Arg Ala Asp Pro Ala Phe Val Cys Arg Gln	
270 275 280 285	
gga gtg gtg gac agg ggc tgg ggc aac ggc tgc gga cta ttt ggc aaa	1813
Gly Val Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys	
290 295 300	
gga agc att gac aca tgc gcc aaa ttt gcc tgc tct acc aag gca ata	1861
Gly Ser Ile Asp Thr Cys Ala Lys Phe Ala Cys Ser Thr Lys Ala Ile	
305 310 315	

gga aga acc atc ttg aaa gag aat atc aag tac gaa gtg gcc att ttt Gly Arg Thr Ile Leu Lys Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe 320 325 330	1909
gtc cat gga cca act act gtg gag tcg cac gga aac tac tcc aca cag Val His Gly Pro Thr Thr Val Glu Ser His Gly Asn Tyr Ser Thr Gln 335 340 345	1957
gtt gga gcc act cag gca ggg aga ttc agc atc act cct gcg gcg cct Val Gly Ala Thr Gln Ala Gly Arg Phe Ser Ile Thr Pro Ala Ala Pro 350 355 360 365	2005
tca tac aca cta aag ctt gga gaa tat gga gag gtg aca gtg gac tgt Ser Tyr Thr Leu Lys Leu Gly Glu Tyr Gly Glu Val Thr Val Asp Cys 370 375 380	2053
gaa cca cgg tca ggg att gac acc aat gca tac tac gtg atg act gtt Glu Pro Arg Ser Gly Ile Asp Thr Asn Ala Tyr Tyr Val Met Thr Val 385 390 395	2101
gga aca aag acg ttc ttg gtc cat cgt gag tgg ttc atg gac ctc aac Gly Thr Lys Thr Phe Leu Val His Arg Glu Trp Phe Met Asp Leu Asn 400 405 410	2149
ctc cct tgg agc agt gct gga agt act gtg tgg agg aac aga gag acg Leu Pro Trp Ser Ser Ala Gly Ser Thr Val Trp Arg Asn Arg Glu Thr 415 420 425	2197
tta atg gag ttt gag gaa cca cac gcc acg aag cag tct gtg ata gca Leu Met Glu Phe Glu Glu Pro His Ala Thr Lys Gln Ser Val Ile Ala 430 435 440 445	2245
ttg ggc tca caa gag gga gct ctg cat caa gct ttg gct gga gcc att Leu Gly Ser Gln Glu Gly Ala Leu His Gln Ala Leu Ala Gly Ala Ile 450 455 460	2293
cct gtg gaa ttt tca agc aac act gtc aag ttg acg tcg ggt cat ttg Pro Val Glu Phe Ser Ser Asn Thr Val Lys Leu Thr Ser Gly His Leu 465 470 475	2341
aag tgt aga gtg aag atg gaa aaa ttg cag ttg aag gga aca acc tat Lys Cys Arg Val Lys Met Glu Lys Leu Gln Leu Lys Gly Thr Thr Tyr 480 485 490	2389
ggc gtc tgt tca aag gct ttc aag ttt ctt ggg act ccc gcg gac aca Gly Val Cys Ser Lys Ala Phe Lys Phe Leu Gly Thr Pro Ala Asp Thr 495 500 505	2437
ggg cac ggc act gtg gtg ttg gaa ttg cag tac act ggc acg gat gga Gly His Gly Thr Val Val Leu Glu Leu Gln Tyr Thr Gly Thr Asp Gly 510 515 520 525	2485
cct tgc aaa gtt cct atc tcg tca gtg gct tca ttg aac gac cta acg Pro Cys Lys Val Pro Ile Ser Ser Val Ala Ser Leu Asn Asp Leu Thr 530 535 540	2533

cca gtg ggc aga ttg gtc act gtc aac cct ttt gtt tca gtg gcc acg	2581
Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ser Val Ala Thr	
545 550 555	
gcc aac gct aag gtc ctg att gaa ttg gaa cca ccc ttt gga gac tca	2629
Ala Asn Ala Lys Val Leu Ile Glu Leu Glu Pro Pro Phe Gly Asp Ser	
560 565 570	
tac ata gtg gtg ggc aga gga gaa caa cag atc aat cac cat tgg cac	2677
Tyr Ile Val Val Gly Arg Gly Glu Gln Gln Ile Asn His His Trp His	
575 580 585	
aag tct gga agc agc att ggc aaa gcc ttt aca acc acc ctc aaa gga	2725
Lys Ser Gly Ser Ser Ile Gly Lys Ala Phe Thr Thr Thr Leu Lys Gly	
590 595 600 605	
gcg cag aga cta gcc gct cta gga gac aca gct tgg gac ttt gga tca	2773
Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser	
610 615 620	
gtt gga ggg gtg ttc acc tca gtt ggg aag gct gtc cat caa gtg ttc	2821
Val Gly Gly Val Phe Thr Ser Val Gly Lys Ala Val His Gln Val Phe	
625 630 635	
gga gga gca ttc cgc tca ctg ttc gga ggc atg tcc tgg ata acg caa	2869
Gly Gly Ala Phe Arg Ser Leu Phe Gly Gly Met Ser Trp Ile Thr Gln	
640 645 650	
gga ttg ctg ggg gct ctc ctg ttg tgg atg ggc atc aat gct cgt gat	2917
Gly Leu Leu Gly Ala Leu Leu Leu Trp Met Gly Ile Asn Ala Arg Asp	
655 660 665	
agg tcc ata gct ctc acg ttt ctc gca gtt gga gga gtt ctg ctc ttc	2965
Arg Ser Ile Ala Leu Thr Phe Leu Ala Val Gly Gly Val Leu Leu Phe	
670 675 680 685	
ctc tcc gtg aac gtg cac gcc t gaaggcggcc gctcgagcat gcatctagag	3017
Leu Ser Val Asn Val His Ala	
690	
ggccctattc tatagtgtca cctaaatgct agagctcgct gatcagcctc gactgtgcct	3077
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gccactccca ctgtcctttc ctaataaaaat gaggaaattg catcgcatgtg tctgagtagg	3197
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cgctttctca tagctcacgc tgtaggtatc tcagttcggg ttaggtcgtt cgctccaagc	3797
tgggctgtgt gcacgaaccc cccgttcagc ccgaccgctg cgccttatcc ggtaactatc	3857
gtcttgagtc caacccggta agacacgact tatcgccact ggcagcagcc actggtaaca	3917

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tcctttttca atattattga agcatttatc agggttattg tctcatgagc ggatacatat 5237
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<210> 16

<211> 692

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<223> pCBWN

<400> 16

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Lys Val Met Thr Val Asn Ala Thr Asp Val Thr Asp Val Ile Thr
35          40          45
Ile Pro Thr Ala Ala Gly Lys Asn Leu Cys Ile Val Arg Ala Met Asp
50          55          60
Val Gly Tyr Met Cys Asp Asp Thr Ile Thr Tyr Glu Cys Pro Val Leu
65          70          75          80
Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Thr Lys Ser
85          90          95
Ala Val Tyr Val Arg Tyr Gly Arg Cys Thr Lys Thr Arg His Ser Arg
100         105         110
Arg Ser Arg Arg Ser Leu Thr Val Gln Thr His Gly Glu Ser Thr Leu
115         120         125
Ala Asn Lys Lys Gly Ala Trp Met Asp Ser Thr Lys Ala Thr Arg Tyr
130         135         140
Leu Val Lys Thr Glu Ser Trp Ile Leu Arg Asn Pro Gly Tyr Ala Leu
145         150         155         160

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Val	Ala	Ala	Val	Ile	Gly	Trp	Met	Leu	Gly	Ser	Asn	Thr	Met	Gln	Arg
				165					170					175	
Val	Val	Phe	Val	Val	Leu	Leu	Leu	Leu	Val	Ala	Pro	Ala	Tyr	Ser	Phe
			180					185					190		
Asn	Cys	Leu	Gly	Met	Ser	Asn	Arg	Asp	Phe	Leu	Glu	Gly	Val	Ser	Gly
		195					200					205			
Ala	Thr	Trp	Val	Asp	Leu	Val	Leu	Glu	Gly	Asp	Ser	Cys	Val	Thr	Ile
	210					215					220				
Met	Ser	Lys	Asp	Lys	Pro	Thr	Ile	Asp	Val	Lys	Met	Met	Asn	Met	Glu
225					230					235					240
Ala	Ala	Asn	Leu	Ala	Glu	Val	Arg	Ser	Tyr	Cys	Tyr	Leu	Ala	Thr	Val
			245						250					255	
Ser	Asp	Leu	Ser	Thr	Lys	Ala	Ala	Cys	Pro	Thr	Met	Gly	Glu	Ala	His
		260						265					270		
Asn	Asp	Lys	Arg	Ala	Asp	Pro	Ala	Phe	Val	Cys	Arg	Gln	Gly	Val	Val
		275					280					285			
Asp	Arg	Gly	Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly	Lys	Gly	Ser	Ile
	290					295					300				
Asp	Thr	Cys	Ala	Lys	Phe	Ala	Cys	Ser	Thr	Lys	Ala	Ile	Gly	Arg	Thr
305					310					315					320
Ile	Leu	Lys	Glu	Asn	Ile	Lys	Tyr	Glu	Val	Ala	Ile	Phe	Val	His	Gly
			325						330					335	
Pro	Thr	Thr	Val	Glu	Ser	His	Gly	Asn	Tyr	Ser	Thr	Gln	Val	Gly	Ala
			340					345					350		
Thr	Gln	Ala	Gly	Arg	Phe	Ser	Ile	Thr	Pro	Ala	Ala	Pro	Ser	Tyr	Thr
		355					360					365			
Leu	Lys	Leu	Gly	Glu	Tyr	Gly	Glu	Val	Thr	Val	Asp	Cys	Glu	Pro	Arg
	370					375					380				
Ser	Gly	Ile	Asp	Thr	Asn	Ala	Tyr	Tyr	Val	Met	Thr	Val	Gly	Thr	Lys
385					390					395					400
Thr	Phe	Leu	Val	His	Arg	Glu	Trp	Phe	Met	Asp	Leu	Asn	Leu	Pro	Trp
			405						410					415	
Ser	Ser	Ala	Gly	Ser	Thr	Val	Trp	Arg	Asn	Arg	Glu	Thr	Leu	Met	Glu
		420						425					430		
Phe	Glu	Glu	Pro	His	Ala	Thr	Lys	Gln	Ser	Val	Ile	Ala	Leu	Gly	Ser
		435					440					445			
Gln	Glu	Gly	Ala	Leu	His	Gln	Ala	Leu	Ala	Gly	Ala	Ile	Pro	Val	Glu
	450					455					460				
Phe	Ser	Ser	Asn	Thr	Val	Lys	Leu	Thr	Ser	Gly	His	Leu	Lys	Cys	Arg
465					470					475					480
Val	Lys	Met	Glu	Lys	Leu	Gln	Leu	Lys	Gly	Thr	Thr	Tyr	Gly	Val	Cys
			485						490					495	
Ser	Lys	Ala	Phe	Lys	Phe	Leu	Gly	Thr	Pro	Ala	Asp	Thr	Gly	His	Gly
			500					505					510		
Thr	Val	Val	Leu	Glu	Leu	Gln	Tyr	Thr	Gly	Thr	Asp	Gly	Pro	Cys	Lys
		515					520					525			
Val	Pro	Ile	Ser	Ser	Val	Ala	Ser	Leu	Asn	Asp	Leu	Thr	Pro	Val	Gly
	530					535					540				
Arg	Leu	Val	Thr	Val	Asn	Pro	Phe	Val	Ser	Val	Ala	Thr	Ala	Asn	Ala
545					550					555					560
Lys	Val	Leu	Ile	Glu	Leu	Glu	Pro	Pro	Phe	Gly	Asp	Ser	Tyr	Ile	Val
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Val	Gly	Arg	Gly	Glu	Gln	Gln	Ile	Asn	His	His	Trp	His	Lys	Ser	Gly
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Ser	Ser	Ile	Gly	Lys	Ala	Phe	Thr	Thr	Thr	Leu	Lys	Gly	Ala	Gln	Arg
		595					600					605			
Leu	Ala	Ala	Leu	Gly	Asp	Thr	Ala	Trp	Asp	Phe	Gly	Ser	Val	Gly	Gly

610		615		620
Val Phe Thr Ser Val	Gly Lys Ala Val His Gln	Val Phe Gly Gly Ala		
625	630	635	640	
Phe Arg Ser Leu Phe	Gly Gly Met Ser Trp Ile Thr	Gln Gly Leu Leu		
	645	650	655	
Gly Ala Leu Leu Trp	Met Gly Ile Asn Ala Arg Asp	Arg Ser Ile		
	660	665	670	
Ala Leu Thr Phe Leu	Ala Val Gly Gly Val Leu Leu	Phe Leu Ser Val		
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Asn Val His Ala				
690				

<210> 17

<211> 5334

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> CDS

<222> (916)...(3007)

<221> misc_feature

<222> (1)...(5334)

<223> pCBE 1-14

<400> 17

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cgagcaaaat	ttaagctaca	acaaggcaag	gcttgaccga	caattgcatg	aagaatctgc	180
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gattattgac	tagtatttaa	tagtaatcaa	ttacggggtc	attagttcat	agcccatata	300
tggagttccg	cgttacataa	cttacggtaa	atggccccgc	tggctgaccg	cccaacgacc	360
cccgccatt	gacgtcaata	atgacgtatg	ttcccatagt	aacgccata	gggactttcc	420
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ctgcttactg	gcttatcgaa	attaatacga	ctcactatag	ggagacccaa	gcttggtacc	900
tctagagccg	ccgcc atg ggc aga aag	caa aac aaa aga gga gga aat gaa				951
	Met Gly Arg Lys	Gln Asn Lys Arg Gly Gly Asn Glu				
	1	5	10			

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Gly Ser Ile Met Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala	
15	20

gga gcc atg aag ttg tcg aat ttc cag ggg aag ctt ttg atg acc atc	1047
Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile	
30	35

aac aac acg gac att gca gac gtt atc gtg att ccc acc tca aaa gga	1095
Asn Asn Thr Asp Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly	
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Glu Asn Arg Cys Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu	
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Asp Thr Ile Thr Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro	
80 85 90	
gag gat gtg gat tgc tgg tgt gac aac caa gaa gtc tac gtc caa tat	1239
Glu Asp Val Asp Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr	
95 100 105	
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Gly Arg Cys Thr Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val	
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Ser Val Gln Thr His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala	
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Trp Leu Asp Ser Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn	
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Trp Ile Ile Arg Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly	
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Leu Leu Leu Val Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly	
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Asn Arg Asp Phe Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu	
205 210 215 220	
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Val Leu Glu Gly Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro	
225 230 235	
aca ttg gac gtc cgc atg att aac atc gaa gct agc caa ctt gct gag	1671
Thr Leu Asp Val Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu	
240 245 250	
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Val Arg Ser Tyr Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val	
255 260 265	

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agt agc tat gtg tgc aaa caa ggc ttc act gac cgt ggg tgg ggc aac Ser Ser Tyr Val Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn 285 290 295 300	1815
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tcc tgc acc agt aaa gcg att ggg aga aca atc cag cca gaa aac atc Ser Cys Thr Ser Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile 320 325 330	1911
aaa tac gaa gtt ggc att ttt gtg cat gga acc acc act tcg gaa aac Lys Tyr Glu Val Gly Ile Phe Val His Gly Thr Thr Thr Ser Glu Asn 335 340 345	1959
cat ggg aat tat tca gcg caa gtt ggg gcg tcc cag gcg gca aag ttt His Gly Asn Tyr Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe 350 355 360	2007
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gcg ttt tac gtc atg acc gtg ggg tca aag tca ttt ctg gtc cat agg Ala Phe Tyr Val Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg 400 405 410	2151
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cag gcg ttg gca gga gcc atc gtg gtg gag tac tca agc tca gtg aag Gln Ala Leu Ala Gly Ala Ile Val Val Glu Tyr Ser Ser Ser Val Lys 465 470 475	2343
tta aca tca ggc cac ctg aaa tgt agg ctg aaa atg gac aaa ctg gct Leu Thr Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala	2391

480	485	490	
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aaa aat ccg gcg gac act ggt cac gga aca gtt gtc att gaa ctc tcc Lys Asn Pro Ala Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser 510 515 520			2487
tac tct ggg agt gat ggc ccc tgc aaa att ccg att gct tcc gtt gcg Tyr Ser Gly Ser Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala 525 530 535 540			2535
agc ctc aat gac atg acc ccc gtt ggg cgg ctg gtg aca gtg aac ccc Ser Leu Asn Asp Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro 545 550 555			2583
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<210> 18

<211> 697

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<223> pCBE 1-14

<400> 18

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Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile Asn Asn Thr Asp
      35             40             45

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Tyr	Glu	Cys	Pro	Lys	Leu	Thr	Met	Gly	Asn	Asp	Pro	Glu	Asp	Val	Asp
				85					90					95	
Cys	Trp	Cys	Asp	Asn	Gln	Glu	Val	Tyr	Val	Gln	Tyr	Gly	Arg	Cys	Thr
			100					105					110		
Arg	Thr	Arg	His	Ser	Lys	Arg	Ser	Arg	Arg	Ser	Val	Ser	Val	Gln	Thr
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His	Gly	Glu	Ser	Ser	Leu	Val	Asn	Lys	Lys	Glu	Ala	Trp	Leu	Asp	Ser
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Thr	Lys	Ala	Thr	Arg	Tyr	Leu	Met	Lys	Thr	Glu	Asn	Trp	Ile	Ile	Arg
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Asn	Pro	Gly	Tyr	Ala	Phe	Leu	Ala	Ala	Val	Leu	Gly	Trp	Met	Leu	Gly
				165					170					175	
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	195					200						205			
Ile	Glu	Gly	Ala	Ser	Gly	Ala	Thr	Trp	Val	Asp	Leu	Val	Leu	Glu	Gly
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Asp	Ser	Cys	Leu	Thr	Ile	Met	Ala	Asn	Asp	Lys	Pro	Thr	Leu	Asp	Val
225					230					235					240
Arg	Met	Ile	Asn	Ile	Glu	Ala	Ser	Gln	Leu	Ala	Glu	Val	Arg	Ser	Tyr
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Cys	Tyr	His	Ala	Ser	Val	Thr	Asp	Ile	Ser	Thr	Val	Ala	Arg	Cys	Pro
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Thr	Thr	Gly	Glu	Ala	His	Asn	Glu	Lys	Arg	Ala	Asp	Ser	Ser	Tyr	Val
	275						280					285			
Cys	Lys	Gln	Gly	Phe	Thr	Asp	Arg	Gly	Trp	Gly	Asn	Gly	Cys	Gly	Leu
	290					295					300				
Phe	Gly	Lys	Gly	Ser	Ile	Asp	Thr	Cys	Ala	Lys	Phe	Ser	Cys	Thr	Ser
305					310					315					320
Lys	Ala	Ile	Gly	Arg	Thr	Ile	Gln	Pro	Glu	Asn	Ile	Lys	Tyr	Glu	Val
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Ser	Ala	Gln	Val	Gly	Ala	Ser	Gln	Ala	Ala	Lys	Phe	Thr	Val	Thr	Pro
	355						360					365			
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Leu	Asp	Cys	Glu	Pro	Arg	Ser	Gly	Leu	Asn	Thr	Glu	Ala	Phe	Tyr	Val
385					390					395					400
Met	Thr	Val	Gly	Ser	Lys	Ser	Phe	Leu	Val	His	Arg	Glu	Trp	Phe	His
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Asp	Leu	Ala	Leu	Pro	Trp	Thr	Ser	Pro	Ser	Ser	Thr	Ala	Trp	Arg	Asn
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Arg	Glu	Leu	Leu	Met	Glu	Phe	Glu	Glu	Ala	His	Ala	Thr	Lys	Gln	Ser
	435						440					445			
Val	Val	Ala	Leu	Gly	Ser	Gln	Glu	Gly	Gly	Leu	His	Gln	Ala	Leu	Ala
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465					470					475					480
His	Leu	Lys	Cys	Arg	Leu	Lys	Met	Asp	Lys	Leu	Ala	Leu	Lys	Gly	Thr
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Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala Ser Leu Asn Asp					
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Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ala Thr					
545			550		555
Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu Pro Pro Phe Gly					
	565		570		575
Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln Ile Asn His His					
580			585		590
Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe Ser Thr Thr Leu					
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Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe					
610			615		620
Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln					
625			630		635
Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile					
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Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met Gly Val Asn Ala					
660			665		670
Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr Gly Gly Val Leu					
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<210> 19

<211> 5283

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> CDS

<222> (910)...(2965)

<400> 19

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1		5		10		

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Arg Glu Gly Tyr Met Val Met Arg Ala Ser Gly Arg Asp Ala Ala Ser	
35 40 45	
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Gln Val Arg Val Gln Asn Gly Thr Cys Val Ile Leu Ala Thr Asp Met	
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Gly Glu Trp Cys Glu Asp Ser Ile Thr Tyr Ser Cys Val Thr Ile Asp	
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cag gag gaa gaa ccc gtt gac gtg gac tgc ttc tgc cga ggt gtt gat	1191
Gln Glu Glu Glu Pro Val Asp Val Asp Cys Phe Cys Arg Gly Val Asp	
80 85 90	
agg gtt aag tta gag tat gga cgc tgt gga agg caa gct gga tct agg	1239
Arg Val Lys Leu Glu Tyr Gly Arg Cys Gly Arg Gln Ala Gly Ser Arg	
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ggg aaa agg tct gtg gtc att cca aca cat gca caa aaa gac atg gtc	1287
Gly Lys Arg Ser Val Val Ile Pro Thr His Ala Gln Lys Asp Met Val	
115 120 125	
ggg cga ggt cat gca tgg ctt aaa ggt gac aat att cga gat cat gtc	1335
Gly Arg Gly His Ala Trp Leu Lys Gly Asp Asn Ile Arg Asp His Val	
130 135 140	
acc cga gtc gag ggc tgg atg tgg aag aac aag ctt cta act gcc gcc	1383
Thr Arg Val Glu Gly Trp Met Trp Lys Asn Lys Leu Leu Thr Ala Ala	
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att gtg gcc ttg gct tgg ctc atg gtt gat agt tgg atg gcc aga gtg	1431
Ile Val Ala Leu Ala Trp Leu Met Val Asp Ser Trp Met Ala Arg Val	
160 165 170	
act gtc atc ctc ttg gcg ttg agt cta ggg cca gtg tac gcc acg agg	1479
Thr Val Ile Leu Leu Ala Leu Ser Leu Gly Pro Val Tyr Ala Thr Arg	
175 180 185 190	
tgc acg cat ctt gag aac aga gat ttt gtg aca gga act caa ggg acc	1527
Cys Thr His Leu Glu Asn Arg Asp Phe Val Thr Gly Thr Gln Gly Thr	
195 200 205	
acc aga gtg tcc cta gtt ttg gaa ctt gga ggc tgc gtg acc atc aca	1575
Thr Arg Val Ser Leu Val Leu Glu Leu Gly Gly Cys Val Thr Ile Thr	
210 215 220	
gct gag ggc aag cca tcc att gat gta tgg ctc gaa gac att ttt cag	1623
Ala Glu Gly Lys Pro Ser Ile Asp Val Trp Leu Glu Asp Ile Phe Gln	
225 230 235	

gaa agc ccg gct gaa acc aga gaa tac tgc ctg cac gcc aaa ttg acc	1671
Glu Ser Pro Ala Glu Thr Arg Glu Tyr Cys Leu His Ala Lys Leu Thr	
240 245 250	
aac aca aaa gtg gag gct cgc tgt cca acc act gga ccg gcg aca ctt	1719
Asn Thr Lys Val Glu Ala Arg Cys Pro Thr Thr Gly Pro Ala Thr Leu	
255 260 265 270	
ccg gag gag cat cag gct aat atg gtg tgc aag aga gac caa agc gac	1767
Pro Glu Glu His Gln Ala Asn Met Val Cys Lys Arg Asp Gln Ser Asp	
275 280 285	
cgt gga tgg gga aac cac tgc ggg ttt ttt ggg aag ggc agt ata gtg	1815
Arg Gly Trp Gly Asn His Cys Gly Phe Phe Gly Lys Gly Ser Ile Val	
290 295 300	
gct tgt gca aag ttt gaa tgc gag gaa gca aaa aaa gct gtg ggc cac	1863
Ala Cys Ala Lys Phe Glu Cys Glu Glu Ala Lys Lys Ala Val Gly His	
305 310 315	
gtc tat gac tcc aca aag atc acg tat gtt gtc aag gtt gag ccc cac	1911
Val Tyr Asp Ser Thr Lys Ile Thr Tyr Val Val Lys Val Glu Pro His	
320 325 330	
aca ggg gat tac ttg gct gca aat gag acc aat tca aac agg aaa tca	1959
Thr Gly Asp Tyr Leu Ala Ala Asn Glu Thr Asn Ser Asn Arg Lys Ser	
335 340 345 350	
gca cag ttt acg gtg gca tcc gag aaa gtg atc ctg cgg ctc ggc gac	2007
Ala Gln Phe Thr Val Ala Ser Glu Lys Val Ile Leu Arg Leu Gly Asp	
355 360 365	
tat gga gat gtg tcg ctg acg tgt aaa gtg gca agt ggg att gat gtc	2055
Tyr Gly Asp Val Ser Leu Thr Cys Lys Val Ala Ser Gly Ile Asp Val	
370 375 380	
gcc caa act gtg gtg atg tca ctc gac agc agc aag gac cac ctg cct	2103
Ala Gln Thr Val Val Met Ser Leu Asp Ser Ser Lys Asp His Leu Pro	
385 390 395	
tct gca tgg caa gtg cac cgt gac tgg ttt gag gac ttg gcg ctg ccc	2151
Ser Ala Trp Gln Val His Arg Asp Trp Phe Glu Asp Leu Ala Leu Pro	
400 405 410	
tgg aaa cac aag gac aac caa gat tgg aac agt gtg gag aaa ctt gtg	2199
Trp Lys His Lys Asp Asn Gln Asp Trp Asn Ser Val Glu Lys Leu Val	
415 420 425 430	
gaa ttt gga cca cca cat gct gtg aaa atg gat gtt ttc aat ctg ggg	2247
Glu Phe Gly Pro Pro His Ala Val Lys Met Asp Val Phe Asn Leu Gly	
435 440 445	
gac cag acg gct gtg ctg ctc aaa tca ctg gca gga gtt ccg ctg gcc	2295
Asp Gln Thr Ala Val Leu Leu Lys Ser Leu Ala Gly Val Pro Leu Ala	
450 455 460	
agt gtg gag ggc cag aaa tac cac ctg aaa agc ggc cat gtt act tgt	2343

Ser	Val	Glu	Gly	Gln	Lys	Tyr	His	Leu	Lys	Ser	Gly	His	Val	Thr	Cys	
		465					470					475				
gat	gtg	gga	ctg	gaa	aag	ctg	aaa	ctg	aaa	ggc	aca	acc	tac	tcc	atg	2391
Asp	Val	Gly	Leu	Glu	Lys	Leu	Lys	Leu	Lys	Gly	Thr	Thr	Tyr	Ser	Met	
		480					485					490				
tgt	gac	aaa	gca	aag	ttc	aaa	tgg	aag	aga	gtt	cct	gtg	gac	agc	ggc	2439
Cys	Asp	Lys	Ala	Lys	Phe	Lys	Trp	Lys	Arg	Val	Pro	Val	Asp	Ser	Gly	
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cat	gac	aca	gta	gtc	atg	gag	gta	tca	tac	aca	gga	agc	gac	aag	cca	2487
His	Asp	Thr	Val	Val	Met	Glu	Val	Ser	Tyr	Thr	Gly	Ser	Asp	Lys	Pro	
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tgt	cgg	atc	ccg	gtg	cgg	gct	gtg	gca	cat	ggc	gtc	cca	gcg	gtt	aat	2535
Cys	Arg	Ile	Pro	Val	Arg	Ala	Val	Ala	His	Gly	Val	Pro	Ala	Val	Asn	
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gta	gcc	atg	ctc	ata	acc	ccc	aat	cca	acc	att	gaa	aca	aat	ggc	ggc	2583
Val	Ala	Met	Leu	Ile	Thr	Pro	Asn	Pro	Thr	Ile	Glu	Thr	Asn	Gly	Gly	
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				595				600						605		
gaa	cat	gca	tgg	gac	ttt	ggc	tca	gta	ggc	ggg	gta	ctg	tct	tct	gtg	2775
Glu	His	Ala	Trp	Asp	Phe	Gly	Ser	Val	Gly	Gly	Val	Leu	Ser	Ser	Val	
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ggg	aag	gca	atc	cac	acg	gtg	ctg	ggg	gga	gct	ttc	aac	acc	ctt	ttt	2823
Gly	Lys	Ala	Ile	His	Thr	Val	Leu	Gly	Gly	Ala	Phe	Asn	Thr	Leu	Phe	
		625					630					635				
ggg	ggg	gtt	gga	ttc	atc	cct	aag	atg	ctg	ctg	ggg	gtt	gct	ctg	gtc	2871
Gly	Gly	Val	Gly	Phe	Ile	Pro	Lys	Met	Leu	Leu	Gly	Val	Ala	Leu	Val	
		640				645					650					
tgg	ttg	gga	cta	aat	gcc	agg	aat	cca	acg	atg	tcc	atg	acg	ttt	ctt	2919
Trp	Leu	Gly	Leu	Asn	Ala	Arg	Asn	Pro	Thr	Met	Ser	Met	Thr	Phe	Leu	
					660					665					670	
gct	gtg	ggg	gct	ttg	aca	ctg	atg	atg	aca	atg	gga	gtt	ggg	gca	t	2965
Ala	Val	Gly	Ala	Leu	Thr	Leu	Met	Met	Thr	Met	Gly	Val	Gly	Ala		
				675					680					685		

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<210> 20

<211> 681

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<400> 20

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Trp	Leu	Leu	Leu	Asn	Val	Thr	Ser	Glu	Asp	Leu	Gly	Lys	Thr	Phe	Ser
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Val	Gly	Thr	Gly	Asn	Cys	Thr	Thr	Asn	Ile	Leu	Glu	Ala	Lys	Tyr	Trp
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Cys	Pro	Asp	Ser	Met	Glu	Tyr	Asn	Cys	Pro	Asn	Leu	Ser	Pro	Arg	Glu
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Glu	Pro	Asp	Asp	Ile	Asp	Cys	Trp	Cys	Tyr	Gly	Val	Glu	Asn	Val	Arg
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Val	Ala	Tyr	Gly	Lys	Cys	Asp	Ser	Ala	Gly	Arg	Ser	Arg	Arg	Ser	Arg
			100					105						110	
Arg	Ala	Ile	Asp	Leu	Pro	Thr	His	Glu	Asn	His	Gly	Leu	Lys	Thr	Arg
		115					120					125			
Gln	Glu	Lys	Trp	Met	Thr	Gly	Arg	Met	Gly	Glu	Arg	Gln	Leu	Gln	Lys
	130					135					140				
Ile	Glu	Arg	Trp	Phe	Val	Arg	Asn	Pro	Phe	Phe	Ala	Val	Thr	Ala	Leu
145					150					155					160
Thr	Ile	Ala	Tyr	Leu	Val	Gly	Ser	Asn	Met	Thr	Gln	Arg	Val	Val	Ile
				165					170					175	
Ala	Leu	Leu	Val	Leu	Ala	Val	Gly	Pro	Ala	Tyr	Ser	Ala	His	Cys	Ile
			180					185					190		
Gly	Ile	Thr	Asp	Arg	Asp	Phe	Ile	Glu	Gly	Val	His	Gly	Gly	Thr	Trp
	195					200						205			
Val	Ser	Ala	Thr	Leu	Glu	Gln	Asp	Lys	Cys	Val	Thr	Val	Met	Ala	Pro
	210					215					220				
Asp	Lys	Pro	Ser	Leu	Asp	Ile	Ser	Leu	Glu	Thr	Val	Ala	Ile	Asp	Arg
225					230					235					240
Pro	Ala	Glu	Val	Arg	Lys	Val	Cys	Tyr	Asn	Ala	Val	Leu	Thr	His	Val
				245					250					255	
Lys	Ile	Asn	Asp	Lys	Cys	Pro	Ser	Thr	Gly	Glu	Ala	His	Leu	Ala	Glu
			260					265					270		
Glu	Asn	Glu	Gly	Asp	Asn	Ala	Cys	Lys	Arg	Thr	Tyr	Ser	Asp	Arg	Gly
	275					280						285			
Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly	Lys	Gly	Ser	Ile	Val	Ala	Cys
	290					295					300				
Ala	Lys	Phe	Thr	Cys	Ala	Lys	Ser	Met	Ser	Leu	Phe	Glu	Val	Asp	Gln
305					310					315					320
Thr	Lys	Ile	Gln	Tyr	Val	Ile	Arg	Ala	Gln	Leu	His	Val	Gly	Ala	Lys
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Gln	Glu	Asn	Trp	Thr	Thr	Asp	Ile	Lys	Thr	Leu	Lys	Phe	Asp	Ala	Leu
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Ser	Gly	Ser	Gln	Glu	Val	Glu	Phe	Ile	Gly	Tyr	Gly	Lys	Ala	Thr	Leu
	355						360					365			
Glu	Cys	Gln	Val	Gln	Thr	Ala	Val	Asp	Phe	Gly	Asn	Ser	Tyr	Ile	Ala
	370					375					380				
Glu	Met	Glu	Thr	Glu	Ser	Trp	Ile	Val	Asp	Arg	Gln	Trp	Ala	Gln	Asp
385					390					395					400
Leu	Thr	Leu	Pro	Trp	Gln	Ser	Gly	Ser	Gly	Gly	Val	Trp	Arg	Glu	Met
				405					410					415	
His	His	Leu	Val	Glu	Phe	Glu	Pro	Pro	His	Ala	Ala	Thr	Ile	Arg	Val
			420					425					430		
Leu	Ala	Leu	Gly	Asn	Gln	Glu	Gly	Ser	Leu	Lys	Thr	Ala	Leu	Thr	Gly
			435				440					445			
Ala	Met	Arg	Val	Thr	Lys	Asp	Thr	Asn	Asp	Asn	Asn	Leu	Tyr	Lys	Leu
	450					455					460				
His	Gly	Gly	His	Val	Ser	Cys	Arg	Val	Lys	Leu	Ser	Ala	Leu	Thr	Leu
465					470					475					480
Lys	Gly	Thr	Ser	Tyr	Lys	Ile	Cys	Thr	Asp	Lys	Met	Phe	Phe	Val	Lys
				485					490					495	

Asn	Pro	Thr	Asp	Thr	Gly	His	Gly	Thr	Val	Val	Met	Gln	Val	Lys	Val
			500					505					510		
Ser	Lys	Gly	Ala	Pro	Cys	Arg	Ile	Pro	Val	Ile	Val	Ala	Asp	Asp	Leu
		515					520					525			

Thr	Ala	Ala	Ile	Asn	Lys	Gly	Ile	Leu	Val	Thr	Val	Asn	Pro	Ile	Ala
	530					535					540				
Ser	Thr	Asn	Asp	Asp	Glu	Val	Leu	Ile	Glu	Val	Asn	Pro	Pro	Phe	Gly
545					550					555					560
Asp	Ser	Tyr	Ile	Ile	Val	Gly	Arg	Gly	Asp	Ser	Arg	Leu	Thr	Tyr	Gln
			565						570					575	
Trp	His	Lys	Glu	Gly	Ser	Ser	Ile	Gly	Lys	Leu	Phe	Thr	Gln	Thr	Met
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Lys	Gly	Val	Glu	Arg	Leu	Ala	Val	Met	Gly	Asp	Thr	Ala	Trp	Asp	Phe
		595					600					605			
Ser	Ser	Ala	Gly	Gly	Phe	Phe	Thr	Ser	Val	Gly	Lys	Gly	Ile	His	Thr
	610					615					620				
Val	Phe	Gly	Ser	Ala	Phe	Gln	Gly	Leu	Phe	Gly	Gly	Leu	Asn	Trp	Ile
625					630					635					640
Thr	Lys	Val	Ile	Met	Gly	Ala	Val	Leu	Ile	Trp	Val	Gly	Ile	Asn	Thr
			645						650					655	
Arg	Asn	Met	Thr	Met	Ser	Met	Ser	Met	Ile	Leu	Val	Gly	Val	Ile	Met
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<210> 21
 <211> 5304
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note =
 synthetic construct

<221> CDS
 <222> (910)...(2986)

<400> 21

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Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser

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Leu Ala Val Val Ile Ala Gly Thr Ser Ala Leu Gln Leu Ser Thr Tyr			
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cag ggg aaa gtg tta atg tca atc aac aag act gac gct caa agc gcc			1047
Gln Gly Lys Val Leu Met Ser Ile Asn Lys Thr Asp Ala Gln Ser Ala			
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ata aac att cct agt gcc aac gga gca aac act tgc att gtg agg gct			1095
Ile Asn Ile Pro Ser Ala Asn Gly Ala Asn Thr Cys Ile Val Arg Ala			
	50	55	60
cta gat gtg ggg gtc atg tgc aaa gat gac atc aca tac ctg tgc cca			1143
Leu Asp Val Gly Val Met Cys Lys Asp Asp Ile Thr Tyr Leu Cys Pro			
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gtg ctt tca gcg gga aat gat ccc gag gac att gac tgt tgg tgt gac			1191
Val Leu Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Asp			
	80	85	90
gtc gaa gag gtg tgg gtg cac tac ggc aga tgc acg cgc atg gga cat			1239
Val Glu Glu Val Trp Val His Tyr Gly Arg Cys Thr Arg Met Gly His			
	95	100	110
tcg agg cgt agc cga cgg tca atc tct gtg cag cat cat gga gat tcc			1287
Ser Arg Arg Ser Arg Arg Ser Ile Ser Val Gln His His Gly Asp Ser			
	115	120	125
aca ctg gca aca aag aac acg cca tgg ttg gac acc gtg aaa acc acc			1335
Thr Leu Ala Thr Lys Asn Thr Pro Trp Leu Asp Thr Val Lys Thr Thr			
	130	135	140
aaa tac ttg aca aaa gta gaa aac tgg gtt ttg cgc aat cct gga tat			1383
Lys Tyr Leu Thr Lys Val Glu Asn Trp Val Leu Arg Asn Pro Gly Tyr			
	145	150	155
gcc cta gtt gcg ctg gcg att gga tgg atg ctc ggt agc aac aac aca			1431
Ala Leu Val Ala Leu Ala Ile Gly Trp Met Leu Gly Ser Asn Asn Thr			
	160	165	170
cag aga gtg gtt ttt gtg atc atg ctg atg ctg att gct ccg gca tac			1479
Gln Arg Val Val Phe Val Ile Met Leu Met Leu Ile Ala Pro Ala Tyr			
	175	180	185
agc ttc aac tgt ctg gga aca tca aac agg gac ttt gtc gag gga gcc			1527
Ser Phe Asn Cys Leu Gly Thr Ser Asn Arg Asp Phe Val Glu Gly Ala			
	195	200	205
agt ggg gca aca tgg att gac ttg gta ctt gaa ggg gga agc tgt gtc			1575
Ser Gly Ala Thr Trp Ile Asp Leu Val Leu Glu Gly Gly Ser Cys Val			
	210	215	220
aca gtg atg gca cca gag aaa cca aca ctg gac ttc aaa gtg atg aag			1623
Thr Val Met Ala Pro Glu Lys Pro Thr Leu Asp Phe Lys Val Met Lys			
	225	230	235

atg gag gct acc gag tta gcc act gtg cgt gag tat tgt tac gaa gca	1671
Met Glu Ala Thr Glu Leu Ala Thr Val Arg Glu Tyr Cys Tyr Glu Ala	
240 245 250	
acc ttg gac acg ctg tca aca gtg gca agg tgc ccc aca aca gga gaa	1719
Thr Leu Asp Thr Leu Ser Thr Val Ala Arg Cys Pro Thr Thr Gly Glu	
255 260 265 270	
gct cac aac acc aaa agg agt gac cca aca ttt gtc tgc aaa aga gat	1767
Ala His Asn Thr Lys Arg Ser Asp Pro Thr Phe Val Cys Lys Arg Asp	
275 280 285	
gtt gtg gac cgc gga tgg ggt aac gga tgt ggt ctg ttt gga aaa ggg	1815
Val Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly	
290 295 300	
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Ser Ile Asp Thr Cys Ala Lys Phe Thr Cys Lys Asn Lys Ala Thr Gly	
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Lys Thr Ile Leu Arg Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val	
320 325 330	
cat ggt tca acg gac tct acg tca cat ggc aat tac tct gag cag att	1959
His Gly Ser Thr Asp Ser Thr Ser His Gly Asn Tyr Ser Glu Gln Ile	
335 340 345 350	
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Gly Lys Asn Gln Ala Ala Arg Phe Thr Ile Ser Pro Gln Ala Pro Ser	
355 360 365	
ttt acg gcc aac atg ggc gag tat gga aca gtt acc att gat tgt gaa	2055
Phe Thr Ala Asn Met Gly Glu Tyr Gly Thr Val Thr Ile Asp Cys Glu	
370 375 380	
gca aga tca gga atc aac acg gag gat tat tat gtt ttc act gtc aag	2103
Ala Arg Ser Gly Ile Asn Thr Glu Asp Tyr Tyr Val Phe Thr Val Lys	
385 390 395	
gag aag tca tgg cta gtg aac agg gac tgg ttt cac gac ttg aac ctt	2151
Glu Lys Ser Trp Leu Val Asn Arg Asp Trp Phe His Asp Leu Asn Leu	
400 405 410	
cca tgg acg agc cct gcc aca act gat tgg cgc aac aga gaa aca ctg	2199
Pro Trp Thr Ser Pro Ala Thr Thr Asp Trp Arg Asn Arg Glu Thr Leu	
415 420 425 430	
gtg gaa ttt gag gaa ccg cat gcc acc aag caa act gta gta gcc cta	2247
Val Glu Phe Glu Glu Pro His Ala Thr Lys Gln Thr Val Val Ala Leu	
435 440 445	
gga tcg caa gaa ggt gcc ctg cac aca gca ttg gct gga gcc att cca	2295
Gly Ser Gln Glu Gly Ala Leu His Thr Ala Leu Ala Gly Ala Ile Pro	

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Ala	Thr	Val	Ser	Ser	Ser	Thr	Leu	Thr	Leu	Gln	Ser	Gly	His	Leu	Lys															
		465						470				475																		
tgc	aga	gct	aag	ctt	gac	aag	gtc	aaa	atc	aag	gga	acg	aca	tat	ggc		2391													
Cys	Arg	Ala	Lys	Leu	Asp	Lys	Val	Lys	Ile	Lys	Gly	Thr	Thr	Tyr	Gly															
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atg	tgt	gac	tct	gcc	ttc	acc	ttc	agc	aag	aac	cca	act	gac	aca	ggg		2439													
Met	Cys	Asp	Ser	Ala	Phe	Thr	Phe	Ser	Lys	Asn	Pro	Thr	Asp	Thr	Gly															
495					500					505					510															
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His	Gly	Thr	Val	Ile	Val	Glu	Leu	Gln	Tyr	Thr	Gly	Ser	Asn	Gly	Pro															
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tgc	cga	gtt	ccc	atc	tcc	gtg	act	gca	aac	ctc	atg	gat	ttg	aca	ccg		2535													
Cys	Arg	Val	Pro	Ile	Ser	Val	Thr	Ala	Asn	Leu	Met	Asp	Leu	Thr	Pro															
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		545					550						555																	
aac	aac	aag	gtc	atg	atc	gaa	gtt	gaa	cca	ccc	ttt	ggc	gat	tct	tac		2631													
Asn	Asn	Lys	Val	Met	Ile	Glu	Val	Glu	Pro	Pro	Phe	Gly	Asp	Ser	Tyr															
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atc	gtc	gtc	gga	aga	ggc	acc	acc	cag	att	aac	tac	cac	tgg	cac	aaa		2679													
Ile	Val	Val	Gly	Arg	Gly	Thr	Thr	Gln	Ile	Asn	Tyr	His	Trp	His	Lys															
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gag	gga	agc	agc	att	ggg	aag	gct	ttg	gcg	acc	aca	tgg	aaa	gga	gcc		2727													
Glu	Gly	Ser	Ser	Ile	Gly	Lys	Ala	Leu	Ala	Thr	Thr	Trp	Lys	Gly	Ala															
				595					600					605																
caa	cgg	cta	gcc	gtc	tta	ggg	gac	aca	gcg	tgg	gac	ttt	gga	tct	att		2775													
Gln	Arg	Leu	Ala	Val	Leu	Gly	Asp	Thr	Ala	Trp	Asp	Phe	Gly	Ser	Ile															
			610					615					620																	
gga	gga	gtt	ttc	aat	tca	att	ggc	aaa	gct	gtc	cac	caa	gtt	ttc	gga		2823													
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Gly	Ala	Phe	Arg	Thr	Leu	Phe	Gly	Gly	Met	Ser	Trp	Ile	Thr	Gln	Gly															
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cta	ctt	gga	gct	ctt	ctc	ctg	tgg	atg	ggg	ttg	cag	gcc	cgc	gac	agg		2919													
Leu	Leu	Gly	Ala	Leu	Leu	Leu	Trp	Met	Gly	Leu	Gln	Ala	Arg	Asp	Arg															
655					660					665					670															
agc	atc	tcg	ctg	act	cta	ctg	gct	gtc	gga	ggg	att	ctc	atc	ttt	ctg		2967													

Ser Ile Ser Leu Thr Leu Leu Ala Val Gly Gly Ile Leu Ile Phe Leu
675 680 685

gca acc agc gtg caa gcc t gagcggccgc tcgagcatgc atctagaggg 3016
Ala Thr Ser Val Gln Ala
690

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<210> 22
<211> 692
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<400> 22

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			20					25					30		
Lys	Val	Leu	Met	Ser	Ile	Asn	Lys	Thr	Asp	Ala	Gln	Ser	Ala	Ile	Asn
		35					40					45			
Ile	Pro	Ser	Ala	Asn	Gly	Ala	Asn	Thr	Cys	Ile	Val	Arg	Ala	Leu	Asp
		50				55					60				
Val	Gly	Val	Met	Cys	Lys	Asp	Asp	Ile	Thr	Tyr	Leu	Cys	Pro	Val	Leu
65					70					75					80
Ser	Ala	Gly	Asn	Asp	Pro	Glu	Asp	Ile	Asp	Cys	Trp	Cys	Asp	Val	Glu
				85					90					95	
Glu	Val	Trp	Val	His	Tyr	Gly	Arg	Cys	Thr	Arg	Met	Gly	His	Ser	Arg
			100					105					110		
Arg	Ser	Arg	Arg	Ser	Ile	Ser	Val	Gln	His	His	Gly	Asp	Ser	Thr	Leu
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Ala	Thr	Lys	Asn	Thr	Pro	Trp	Leu	Asp	Thr	Val	Lys	Thr	Thr	Lys	Tyr
						135					140				
Leu	Thr	Lys	Val	Glu	Asn	Trp	Val	Leu	Arg	Asn	Pro	Gly	Tyr	Ala	Leu
145					150					155					160
Val	Ala	Leu	Ala	Ile	Gly	Trp	Met	Leu	Gly	Ser	Asn	Asn	Thr	Gln	Arg
				165					170					175	
Val	Val	Phe	Val	Ile	Met	Leu	Met	Leu	Ile	Ala	Pro	Ala	Tyr	Ser	Phe
			180					185					190		
Asn	Cys	Leu	Gly	Thr	Ser	Asn	Arg	Asp	Phe	Val	Glu	Gly	Ala	Ser	Gly
		195					200					205			
Ala	Thr	Trp	Ile	Asp	Leu	Val	Leu	Glu	Gly	Gly	Ser	Cys	Val	Thr	Val
		210				215					220				
Met	Ala	Pro	Glu	Lys	Pro	Thr	Leu	Asp	Phe	Lys	Val	Met	Lys	Met	Glu
225					230					235					240
Ala	Thr	Glu	Leu	Ala	Thr	Val	Arg	Glu	Tyr	Cys	Tyr	Glu	Ala	Thr	Leu
				245					250					255	
Asp	Thr	Leu	Ser	Thr	Val	Ala	Arg	Cys	Pro	Thr	Thr	Gly	Glu	Ala	His
			260					265					270		
Asn	Thr	Lys	Arg	Ser	Asp	Pro	Thr	Phe	Val	Cys	Lys	Arg	Asp	Val	Val
		275					280					285			
Asp	Arg	Gly	Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly	Lys	Gly	Ser	Ile
		290				295					300				
Asp	Thr	Cys	Ala	Lys	Phe	Thr	Cys	Lys	Asn	Lys	Ala	Thr	Gly	Lys	Thr
305					310					315					320
Ile	Leu	Arg	Glu	Asn	Ile	Lys	Tyr	Glu	Val	Ala	Ile	Phe	Val	His	Gly
				325					330					335	
Ser	Thr	Asp	Ser	Thr	Ser	His	Gly	Asn	Tyr	Ser	Glu	Gln	Ile	Gly	Lys
			340					345					350		
Asn	Gln	Ala	Ala	Arg	Phe	Thr	Ile	Ser	Pro	Gln	Ala	Pro	Ser	Phe	Thr
		355					360					365			
Ala	Asn	Met	Gly	Glu	Tyr	Gly	Thr	Val	Thr	Ile	Asp	Cys	Glu	Ala	Arg
		370				375					380				
Ser	Gly	Ile	Asn	Thr	Glu	Asp	Tyr	Tyr	Val	Phe	Thr	Val	Lys	Glu	Lys
385					390					395					400
Ser	Trp	Leu	Val	Asn	Arg	Asp	Trp	Phe	His	Asp	Leu	Asn	Leu	Pro	Trp
				405					410					415	
Thr	Ser	Pro	Ala	Thr	Thr	Asp	Trp	Arg	Asn	Arg	Glu	Thr	Leu	Val	Glu
			420					425					430		
Phe	Glu	Glu	Pro	His	Ala	Thr	Lys	Gln	Thr	Val	Val	Ala	Leu	Gly	Ser
		435					440					445			
Gln	Glu	Gly	Ala	Leu	His	Thr	Ala	Leu	Ala	Gly	Ala	Ile	Pro	Ala	Thr

450		455		460	
Val Ser Ser Ser Thr	Leu Thr Leu Gln Ser Gly	His Leu Lys Cys Arg			
465	470	475	480		
Ala Lys Leu Asp Lys	Val Lys Ile Lys Gly Thr Thr Tyr Gly	Met Cys			
	485	490	495		
Asp Ser Ala Phe Thr	Phe Ser Lys Asn Pro Thr Asp Thr Gly	His Gly			
	500	505	510		
Thr Val Ile Val Glu	Leu Gln Tyr Thr Gly Ser Asn Gly	Pro Cys Arg			
	515	520	525		
Val Pro Ile Ser Val	Thr Ala Asn Leu Met Asp Leu Thr Pro	Val Gly			
	530	535	540		
Arg Leu Val Thr Val	Asn Pro Phe Ile Ser Thr Gly Gly	Ala Asn Asn			
545	550	555	560		
Lys Val Met Ile Glu	Val Glu Pro Pro Phe Gly Asp Ser Tyr	Ile Val			
	565	570	575		
Val Gly Arg Gly Thr	Thr Gln Ile Asn Tyr His Trp His Lys	Glu Gly			
	580	585	590		
Ser Ser Ile Gly Lys	Ala Leu Ala Thr Thr Trp Lys Gly	Ala Gln Arg			
	595	600	605		
Leu Ala Val Leu Gly	Asp Thr Ala Trp Asp Phe Gly Ser Ile	Gly Gly			
	610	615	620		
Val Phe Asn Ser Ile	Gly Lys Ala Val His Gln Val Phe Gly	Gly Ala			
625	630	635	640		
Phe Arg Thr Leu Phe	Gly Gly Met Ser Trp Ile Thr Gln Gly	Leu Leu			
	645	650	655		
Gly Ala Leu Leu Trp	Met Gly Leu Gln Ala Arg Asp Arg Ser	Ile			
	660	665	670		
Ser Leu Thr Leu Leu	Ala Val Gly Gly Ile Leu Ile Phe Leu	Ala Thr			
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Ser Val Gln Ala					
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<210> 23

<211> 5271

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> CDS

<222> (910)...(2953)

<400> 23

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gattattgac	tagttattaa	tagtaatcaa	ttacggggtc	attagttcat	agcccatata	300
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atgccagta	catgacctta	tgggactttc	ctacttgcca	gtacatctac	gtattagtca	600
tcgctattac	catgggtgatg	cggttttggc	agtacatcaa	tgggcgtgga	tagcggtttg	660
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Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser	
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Leu Ala Val Val Ile Ala Gly Thr Ser Ala Val Thr Leu Val Arg Lys	
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Asn Arg Trp Leu Leu Leu Asn Val Thr Ser Glu Asp Leu Gly Lys Thr	
35 40 45	
ttc tct gtg ggc aca ggc aac tgc aca aca aac att ttg gaa gcc aag	1095
Phe Ser Val Gly Thr Gly Asn Cys Thr Thr Asn Ile Leu Glu Ala Lys	
50 55 60	
tac tgg tgc cca gac tca atg gaa tac aac tgt ccc aat ctc agt cca	1143
Tyr Trp Cys Pro Asp Ser Met Glu Tyr Asn Cys Pro Asn Leu Ser Pro	
65 70 75	
aga gag gag cca gat gac att gat tgc tgg tgc tat ggg gtg gaa aac	1191
Arg Glu Glu Pro Asp Asp Ile Asp Cys Trp Cys Tyr Gly Val Glu Asn	
80 85 90	
gtt aga gtc gca tat ggt aag tgt gac tca gca ggc agg tct agg agg	1239
Val Arg Val Ala Tyr Gly Lys Cys Asp Ser Ala Gly Arg Ser Arg Arg	
95 100 105 110	
tca aga agg gcc att gac ttg cct acg cat gaa aac cat ggt ttg aag	1287
Ser Arg Arg Ala Ile Asp Leu Pro Thr His Glu Asn His Gly Leu Lys	
115 120 125	
acc cgg caa gaa aaa tgg atg act gga aga atg ggt gaa agg caa ctc	1335
Thr Arg Gln Glu Lys Trp Met Thr Gly Arg Met Gly Glu Arg Gln Leu	
130 135 140	
caa aag att gag aga tgg ttc gtg agg aac ccc ttt ttt gca gtg acg	1383
Gln Lys Ile Glu Arg Trp Phe Val Arg Asn Pro Phe Phe Ala Val Thr	
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Val Ile Ala Leu Leu Val Leu Ala Val Gly Pro Ala Tyr Ser Ala His	
175 180 185 190	
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Cys Ile Gly Ile Thr Asp Arg Asp Phe Ile Glu Gly Val His Gly Gly	
195 200 205	

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Thr Trp Val Ser Ala Thr Leu Glu Gln Asp Lys Cys Val Thr Val Met	
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Ala Pro Asp Lys Pro Ser Leu Asp Ile Ser Leu Glu Thr Val Ala Ile	
225 230 235	
gat aga cct gct gag gtg agg aaa gtg tgt tac aat gca gtt ctc act	1671
Asp Arg Pro Ala Glu Val Arg Lys Val Cys Tyr Asn Ala Val Leu Thr	
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His Val Lys Ile Asn Asp Lys Cys Pro Ser Thr Gly Glu Ala His Leu	
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Ala Glu Glu Asn Glu Gly Asp Asn Ala Cys Lys Arg Thr Tyr Ser Asp	
275 280 285	
aga ggc tgg ggc aat ggc tgt ggc cta ttt ggg aaa ggg agc att gtg	1815
Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Val	
290 295 300	
gca tgc gcc aaa ttc act tgt gcc aaa tcc atg agt ttg ttt gag gtt	1863
Ala Cys Ala Lys Phe Thr Cys Ala Lys Ser Met Ser Leu Phe Glu Val	
305 310 315	
gat cag acc aaa att cag tat gtc atc aga gca caa ttg cat gta ggg	1911
Asp Gln Thr Lys Ile Gln Tyr Val Ile Arg Ala Gln Leu His Val Gly	
320 325 330	
gcc aag cag gaa aat tgg act acc gac att aag act ctc aag ttt gat	1959
Ala Lys Gln Glu Asn Trp Thr Thr Asp Ile Lys Thr Leu Lys Phe Asp	
335 340 345 350	
gcc ctg tca ggc tcc cag gaa gtc gag ttc att ggg tat gga aaa gct	2007
Ala Leu Ser Gly Ser Gln Glu Val Glu Phe Ile Gly Tyr Gly Lys Ala	
355 360 365	
aca ctg gaa tgc cag gtg caa act gcg gtg gac ttt ggt aac agt tac	2055
Thr Leu Glu Cys Gln Val Gln Thr Ala Val Asp Phe Gly Asn Ser Tyr	
370 375 380	
atc gct gag atg gaa aca gag agc tgg ata gtg gac aga cag tgg gcc	2103
Ile Ala Glu Met Glu Thr Glu Ser Trp Ile Val Asp Arg Gln Trp Ala	
385 390 395	
cag gac ttg acc ctg cca tgg cag agt gga agt ggc ggg gtg tgg aga	2151
Gln Asp Leu Thr Leu Pro Trp Gln Ser Gly Ser Gly Gly Val Trp Arg	
400 405 410	
gag atg cat cat ctt gtc gaa ttt gaa cct ccg cat gcc gcc act atc	2199
Glu Met His His Leu Val Glu Phe Glu Pro Pro His Ala Ala Thr Ile	
415 420 425 430	

aga gta ctg gcc ctg gga aac cag gaa ggc tcc ttg aaa aca gct ctt	2247
Arg Val Leu Ala Leu Gly Asn Gln Glu Gly Ser Leu Lys Thr Ala Leu	
435 440 445	
act ggc gca atg agg gtt aca aag gac aca aat gac aac aac ctt tac	2295
Thr Gly Ala Met Arg Val Thr Lys Asp Thr Asn Asp Asn Asn Leu Tyr	
450 455 460	
aaa cta cat ggt gga cat gtt tct tgc aga gtg aaa ttg tca gct ttg	2343
Lys Leu His Gly Gly His Val Ser Cys Arg Val Lys Leu Ser Ala Leu	
465 470 475	
aca ctc aag ggg aca tcc tac aaa ata tgc act gac aaa atg ttt ttt	2391
Thr Leu Lys Gly Thr Ser Tyr Lys Ile Cys Thr Asp Lys Met Phe Phe	
480 485 490	
gtc aag aac cca act gac act ggc cat ggc act gtt gtg atg cag gtg	2439
Val Lys Asn Pro Thr Asp Thr Gly His Gly Thr Val Val Met Gln Val	
495 500 505 510	
aaa gtg tca aaa gga gcc ccc tgc agg att cca gtg ata gta gct gat	2487
Lys Val Ser Lys Gly Ala Pro Cys Arg Ile Pro Val Ile Val Ala Asp	
515 520 525	
gat ctt aca gcg gca atc aat aaa ggc att ttg gtt aca gtt aac ccc	2535
Asp Leu Thr Ala Ala Ile Asn Lys Gly Ile Leu Val Thr Val Asn Pro	
530 535 540	
atc gcc tca acc aat gat gat gaa gtg ctg att gag gtg aac cca cct	2583
Ile Ala Ser Thr Asn Asp Asp Glu Val Leu Ile Glu Val Asn Pro Pro	
545 550 555	
ttt gga gac agc tac att atc gtt ggg aga gga gat tca cgt ctc act	2631
Phe Gly Asp Ser Tyr Ile Ile Val Gly Arg Gly Asp Ser Arg Leu Thr	
560 565 570	
tac cag tgg cac aaa gag gga agc tca ata gga aag ttg ttc act cag	2679
Tyr Gln Trp His Lys Glu Gly Ser Ser Ile Gly Lys Leu Phe Thr Gln	
575 580 585 590	
acc atg aaa ggc gtg gaa cgc ctg gcc gtc atg gga gac acc gcc tgg	2727
Thr Met Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp	
595 600 605	
gat ttc agc tcc gct gga ggg ttc ttc act tcg gtt ggg aaa gga att	2775
Asp Phe Ser Ser Ala Gly Gly Phe Phe Thr Ser Val Gly Lys Gly Ile	
610 615 620	
cat acg gtg ttt ggc tct gcc ttt cag ggg cta ttt ggc ggc ttg aac	2823
His Thr Val Phe Gly Ser Ala Phe Gln Gly Leu Phe Gly Gly Leu Asn	
625 630 635	
tgg ata aca aag gtc atc atg ggg gcg gta ctt ata tgg gtt ggc atc	2871
Trp Ile Thr Lys Val Ile Met Gly Ala Val Leu Ile Trp Val Gly Ile	

640	645	650	
aac aca aga aac atg aca atg tcc atg agc atg	atc ttg gta gga gtg	2919	
Asn Thr Arg Asn Met Thr Met Ser Met Ser Met	Ile Leu Val Gly Val		
655	660 665 670		
atc atg atg ttt ttg tct cta gga gtt ggg gcg	t gagcggccgc	2963	
Ile Met Met Phe Leu Ser Leu Gly Val Gly Ala			
675	680		
tcgagcatgc atctagaggg ccctattcta tagtgtcacc taaatgctag agctcgctga	3023		
tcagcctcga ctgtgccttc tagttgccag ccatctgttg tttgcccctc ccccgctgcct	3083		
tccttgaccc tggaaggtgc cactcccact gtcctttcct aataaaatga ggaaattgca	3143		
tcgcattgtc tgagtaggtg tcattctatt ctgggggggtg ggggtggggca ggacagcaag	3203		
ggggaggatt gggaagacaa tagcaggcat gctggggatg cgggtgggctc tatggcttct	3263		
gaggcgga aaacagctgc attaatgaat cggccaacgc gcggggagag gcggtttgcg	3323		
tattgggctc tcttcgctt cctcgctcac tgactcgctg cgctcggtcg ttcggctgcg	3383		
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cgcaggaaaag aacatgtgag caaaaggcca gcaaaaggcc aggaaccgta aaaaggccgc	3503		
gttgctggcg tttttccata ggctccgccc ccttgacgag catcacaaaa atcgacgctc	3563		
aagtcagagg tggcgaacc cgacaggact ataaagatac caggcgtttc cccctggaag	3623		
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gaagtgggtg cctaactacg gctacactag aaggacagta tttggtatct gcgctctgct	3983		
gaagccagtt accttcgga aaagagttgg tagctcttga tccggcaaac aaaccaccgc	4043		
tggtagcggg ggtttttttg tttgcaagca gcagattacg cgcagaaaaa aaggatctca	4103		
agaagatcct ttgatctttt ctacggggtc tgacgctcag tggaacgaaa actcacgtta	4163		
agggattttg gtcatgagat tatcaaaaag gatcttcacc tagatccttt taaattaaaa	4223		
atgaagtttt aaatcaatct aaagtatata tgagtaaact tggctctgaca gttaccaatg	4283		
cttaatcagt gaggcaccta tctcagcgat ctgtctattt cgttcatcca tagttgcctg	4343		
actccccgtc gtgtagataa ctacgatacg ggagggttta ccatctggcc ccagtgtgc	4403		
aatgataccg cgagaccac gctcaccggc tccagattta tcagcaataa accagccagc	4463		
cggaagggcc gagcgcagaa gtggtcctgc aactttatcc gcctccatcc agtctattaa	4523		
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ggcagcactg cataattctc ttactgtcat gccatccgta agatgcttt ctgtgactgg	4823		
tgagtactca accaagtcac tctgagaata gtgtatgcgg cgaccgagtt gctcttgccc	4883		
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aaaacgttct tcggggcgaa aactctcaag gatcttaccg ctggtgagat ccagttcgat	5003		
gtaaccact cgtgcaccca actgatcttc agcatctttt actttcacca gcgtttctgg	5063		
gtgagcaaaa acaggaaggc aaaatgccgc aaaaaaggga ataaggcgca cacggaaatg	5123		
ttgaatactc atactcttcc tttttcaata ttattgaagc atttatcagg gttattgtct	5183		
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<210> 24

<211> 681

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =

synthetic construct

<400> 24

Met	Gly	Lys	Arg	Ser	Ala	Gly	Ser	Ile	Met	Trp	Leu	Ala	Ser	Leu	Ala
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Val	Val	Ile	Ala	Gly	Thr	Ser	Ala	Val	Thr	Leu	Val	Arg	Lys	Asn	Arg
			20					25					30		
Trp	Leu	Leu	Leu	Asn	Val	Thr	Ser	Glu	Asp	Leu	Gly	Lys	Thr	Phe	Ser
		35					40					45			
Val	Gly	Thr	Gly	Asn	Cys	Thr	Thr	Asn	Ile	Leu	Glu	Ala	Lys	Tyr	Trp
	50					55					60				
Cys	Pro	Asp	Ser	Met	Glu	Tyr	Asn	Cys	Pro	Asn	Leu	Ser	Pro	Arg	Glu
65					70				75						80
Glu	Pro	Asp	Asp	Ile	Asp	Cys	Trp	Cys	Tyr	Gly	Val	Glu	Asn	Val	Arg
				85					90					95	
Val	Ala	Tyr	Gly	Lys	Cys	Asp	Ser	Ala	Gly	Arg	Ser	Arg	Arg	Ser	Arg
			100					105					110		
Arg	Ala	Ile	Asp	Leu	Pro	Thr	His	Glu	Asn	His	Gly	Leu	Lys	Thr	Arg
	115						120					125			
Gln	Glu	Lys	Trp	Met	Thr	Gly	Arg	Met	Gly	Glu	Arg	Gln	Leu	Gln	Lys
	130					135					140				
Ile	Glu	Arg	Trp	Phe	Val	Arg	Asn	Pro	Phe	Phe	Ala	Val	Thr	Ala	Leu
145					150				155						160
Thr	Ile	Ala	Tyr	Leu	Val	Gly	Ser	Asn	Met	Thr	Gln	Arg	Val	Val	Ile
				165					170					175	
Ala	Leu	Leu	Val	Leu	Ala	Val	Gly	Pro	Ala	Tyr	Ser	Ala	His	Cys	Ile
			180					185					190		
Gly	Ile	Thr	Asp	Arg	Asp	Phe	Ile	Glu	Gly	Val	His	Gly	Gly	Thr	Trp
	195						200					205			
Val	Ser	Ala	Thr	Leu	Glu	Gln	Asp	Lys	Cys	Val	Thr	Val	Met	Ala	Pro
	210					215					220				
Asp	Lys	Pro	Ser	Leu	Asp	Ile	Ser	Leu	Glu	Thr	Val	Ala	Ile	Asp	Arg
225					230				235						240
Pro	Ala	Glu	Val	Arg	Lys	Val	Cys	Tyr	Asn	Ala	Val	Leu	Thr	His	Val
				245					250					255	
Lys	Ile	Asn	Asp	Lys	Cys	Pro	Ser	Thr	Gly	Glu	Ala	His	Leu	Ala	Glu
			260					265					270		
Glu	Asn	Glu	Gly	Asp	Asn	Ala	Cys	Lys	Arg	Thr	Tyr	Ser	Asp	Arg	Gly
	275						280					285			
Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly	Lys	Gly	Ser	Ile	Val	Ala	Cys
	290					295					300				
Ala	Lys	Phe	Thr	Cys	Ala	Lys	Ser	Met	Ser	Leu	Phe	Glu	Val	Asp	Gln
305					310					315					320
Thr	Lys	Ile	Gln	Tyr	Val	Ile	Arg	Ala	Gln	Leu	His	Val	Gly	Ala	Lys
				325					330					335	
Gln	Glu	Asn	Trp	Thr	Thr	Asp	Ile	Lys	Thr	Leu	Lys	Phe	Asp	Ala	Leu
			340					345					350		
Ser	Gly	Ser	Gln	Glu	Val	Glu	Phe	Ile	Gly	Tyr	Gly	Lys	Ala	Thr	Leu
	355						360					365			
Glu	Cys	Gln	Val	Gln	Thr	Ala	Val	Asp	Phe	Gly	Asn	Ser	Tyr	Ile	Ala
	370					375					380				
Glu	Met	Glu	Thr	Glu	Ser	Trp	Ile	Val	Asp	Arg	Gln	Trp	Ala	Gln	Asp
385					390				395						400
Leu	Thr	Leu	Pro	Trp	Gln	Ser	Gly	Ser	Gly	Gly	Val	Trp	Arg	Glu	Met
				405					410					415	
His	His	Leu	Val	Glu	Phe	Glu	Pro	Pro	His	Ala	Ala	Thr	Ile	Arg	Val
			420					425						430	

Leu	Ala	Leu	Gly	Asn	Gln	Glu	Gly	Ser	Leu	Lys	Thr	Ala	Leu	Thr	Gly
		435					440					445			
Ala	Met	Arg	Val	Thr	Lys	Asp	Thr	Asn	Asp	Asn	Asn	Leu	Tyr	Lys	Leu
	450					455				460					
His	Gly	Gly	His	Val	Ser	Cys	Arg	Val	Lys	Leu	Ser	Ala	Leu	Thr	Leu
465					470					475					480
Lys	Gly	Thr	Ser	Tyr	Lys	Ile	Cys	Thr	Asp	Lys	Met	Phe	Phe	Val	Lys
				485					490					495	
Asn	Pro	Thr	Asp	Thr	Gly	His	Gly	Thr	Val	Val	Met	Gln	Val	Lys	Val
			500					505					510		
Ser	Lys	Gly	Ala	Pro	Cys	Arg	Ile	Pro	Val	Ile	Val	Ala	Asp	Asp	Leu
	515						520					525			
Thr	Ala	Ala	Ile	Asn	Lys	Gly	Ile	Leu	Val	Thr	Val	Asn	Pro	Ile	Ala
	530					535					540				
Ser	Thr	Asn	Asp	Asp	Glu	Val	Leu	Ile	Glu	Val	Asn	Pro	Pro	Phe	Gly
545					550					555					560
Asp	Ser	Tyr	Ile	Ile	Val	Gly	Arg	Gly	Asp	Ser	Arg	Leu	Thr	Tyr	Gln
			565						570					575	
Trp	His	Lys	Glu	Gly	Ser	Ser	Ile	Gly	Lys	Leu	Phe	Thr	Gln	Thr	Met
			580					585					590		
Lys	Gly	Val	Glu	Arg	Leu	Ala	Val	Met	Gly	Asp	Thr	Ala	Trp	Asp	Phe
	595						600					605			
Ser	Ser	Ala	Gly	Gly	Phe	Phe	Thr	Ser	Val	Gly	Lys	Gly	Ile	His	Thr
	610				615					620					
Val	Phe	Gly	Ser	Ala	Phe	Gln	Gly	Leu	Phe	Gly	Gly	Leu	Asn	Trp	Ile
625					630					635					640
Thr	Lys	Val	Ile	Met	Gly	Ala	Val	Leu	Ile	Trp	Val	Gly	Ile	Asn	Thr
			645						650					655	
Arg	Asn	Met	Thr	Met	Ser	Met	Ser	Met	Ile	Leu	Val	Gly	Val	Ile	Met
			660				665						670		
Met	Phe	Leu	Ser	Leu	Gly	Val	Gly	Ala							
		675					680								

<210> 25

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> misc_feature

<222> 1-35

<223> POW 454

<400> 25

aaaagaaaaa gcgctaccac catccaccgg gacag

35

<210> 26

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> misc_feature

<222> 1-41

<223> CPOW 2417

<400> 26

actgttacc tcaaccccggt actcgccggc gaaaaagaaa a

41

<210> 27

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<223> Modified JE Signal

<400> 27

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala

1 5 10 15

Val Val Ile Ala Gly Thr Ser Ala

20

<210> 28

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> misc_feature

<222> 1-36

<223> YF 482

<400> 28

aaaagaaaaa gcgctgtgac cttggtgcgg aaaaac

36

<210> 29

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> misc_feature

<222> 1-41

<223> CYF 2433

<400> 29

acagagatcc tcaaccccggt actcgccggc gaaaaagaaa a

41

<210> 30
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<221> misc_feature
<222> 1-41
<223> SLE 463

<400> 30
aaaagaaaaa gcgctttgca gttatcaacc tatcagggga a

41

<210> 31
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<221> misc_feature
<222> 1-40
<223> CSLE 2477

<400> 31
accgttggtc gcacgttcgg actcgccggc gaaaaagaaa

40

<210> 32
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<400> 32
Leu Asp Thr Ile Asn Arg Arg Pro Ser Lys Lys Arg Gly Gly Thr Arg
1 5 10 15
Ser Leu Leu Gly Leu Ala Ala Leu Ile Gly Leu Ala Ser Ser Leu Gln
20 25 30
Leu Leu Ser Thr Tyr Gln Gly
35

<210> 33
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<400> 33
Met Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Met
1 5 10 15
Lys Leu Ser Asn Phe Gln Gly Lys
20

<210> 34
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<400> 34
Met Asn Glu Gly Ser Ile Met Trp Leu Ala Ser Leu Ala Val Val Ile
1 5 10 15
Ala Cys Ala Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys
20 25 30

<210> 35
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<400> 35
Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu Gly Ser Ile Met
1 5 10 15
Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Met Lys
20 25 30
Leu Ser Asn Phe Gln Gly Lys
35

<210> 36
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<400> 36
Met Ser Lys Lys Arg Gly Gly Ser Glu Thr Ser Val Leu Met Val Ile
1 5 10 15
Phe Met Leu Ile Gly Phe Ala Ala Ala Leu Lys Leu Ser Asn Phe Gln
20 25 30
Gly Lys

<210> 37

<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<400> 37
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1 5 10 15
Val Val Ile Ala Cys Ala Gly Ala Val Thr Leu Ser Asn Phe Gln Gly
20 25 30
Lys

<210> 38
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<400> 38
Met Asn Val Leu Arg Gly Phe Arg Lys Glu Ile Gly Arg Met Leu Asn
1 5 10 15
Ile Leu Asn Arg Arg Arg Arg Thr Ala Gly Met Ile Ile Met Leu Ile
20 25 30
Pro Thr Val Met Ala Phe His Leu Thr Thr Arg Asn Gly Glu
35 40 45

<210> 39
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<400> 39
Met Val Gly Leu Gln Lys Arg Gly Lys Arg Arg Ser Ala Thr Asp Trp
1 5 10 15
Met Ser Trp Leu Leu Val Ile Thr Leu Leu Gly Met Thr Leu Ala Ala
20 25 30
Thr Val Arg Lys Glu Arg Gly Asp
35 40

<210> 40
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =

synthetic construct

<400> 40

Met Gly Trp Leu Leu Val Val Val Leu Leu Gly Val Thr Leu Ala Ala
 1 5 10 15
 Thr Val Arg Lys Glu Arg Gly Asp
 20

<210> 41

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
 synthetic construct

<400> 41

Met Ser Trp Leu Leu Val Ile Thr Leu Leu Gly Met Thr Ile Ala Ala
 1 5 10 15
 Thr Val Arg Lys Glu Arg Gly Asp
 20

<210> 42

<211> 5292

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
 synthetic construct

<221> CDS

<222> (910)...(2964)

<400> 42

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cgagcaaaat	ttaagctaca	acaaggcaag	gcttgaccga	caattgcatg	aagaatctgc	180
ttagggttag	gcgttttgcg	ctgcttcgcg	atgtacgggc	cagatatacg	cgttgacatt	240
gattattgac	tagttattaa	tagtaatcaa	ttacggggtc	attagttcat	agcccatata	300
tggagttccg	cgttacataa	cttacggtaa	atggcccggc	tggctgaccg	cccaacgacc	360
cccggccatt	gacgtcaata	atgacgtatg	ttcccatagt	aacgccaata	gggactttcc	420
attgacgtca	atgggtggag	tatttacggt	aaactgcccc	cttggcagta	catcaagtgt	480
atcatatgcc	aagtacgccc	cctattgacg	tcaatgacgg	taaatggccc	gcctggcatt	540
atgcccagta	catgacctta	tgggactttc	ctacttggca	gtacatctac	gtattagtca	600
tcgctattac	catggtgatg	cggtttttggc	agtacatcaa	tgggcgtgga	tagcggtttg	660
actcacgggg	atttccaagt	ctccacccca	ttgacgtcaa	tgggagtttg	ttttggcacc	720
aaaatcaacg	ggactttcca	aaatgtcgta	acaactccgc	cccattgacg	caaatgggcg	780
gtaggcgtgt	acgggtgggag	gtctatataa	gcagagctct	ctggctaact	agagaaccca	840
ctgcttactg	gcttatcgaa	attaatacga	ctcactatag	ggagacccaa	gcttggtacc	900
gccgcccggc	atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc					951
	Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser					
	1 5 10					

ttg gca gtt gtc ata gct tgt gca ggc gcc ttc cat tta acc aca cgt	999
Leu Ala Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg	

15	20	25	30	
aac gga gaa cca cac atg atc gtc agc aga caa gag aaa ggg aaa agt				1047
Asn Gly Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser				
	35	40	45	
ctt ctg ttt aaa aca gag gat ggc gtg aac atg tgt acc ctc atg gcc				1095
Leu Leu Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala				
	50	55	60	
atg gac ctt ggt gaa ttg tgt gaa gac aca atc acg tac aag tgt ccc				1143
Met Asp Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro				
	65	70	75	
ctt ctc agg cag aat gag cca gaa gac ata gac tgt tgg tgc aac tct				1191
Leu Leu Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser				
	80	85	90	
acg tcc acg tgg gta act tat ggg acg tgt acc acc atg gga gaa cat				1239
Thr Ser Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His				
	95	100	105	110
aga aga gaa aaa aga tca gtg gca ctc gtt cca cat gtg gga atg gga				1287
Arg Arg Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly				
	115	120	125	
ctg gag aca cga act gaa aca tgg atg tca tca gaa ggg gcc tgg aaa				1335
Leu Glu Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys				
	130	135	140	
cat gtc cag aga att gaa act tgg atc ttg aga cat cca ggc ttc acc				1383
His Val Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr				
	145	150	155	
atg atg gca gca atc ctg gca tac acc ata gga acg aca cat ttc caa				1431
Met Met Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln				
	160	165	170	
aga gcc ctg att ttc atc tta ctg aca gct gtc act cct tca atg aca				1479
Arg Ala Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr				
	175	180	185	190
atg cgt tgc ata gga atg tca aat aga gac ttt gtg gaa ggg gtt tca				1527
Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser				
	195	200	205	
gga gga agc tgg gtt gac ata gtc tta gaa cat gga agc tgt gtg acg				1575
Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr				
	210	215	220	
acg atg gca aaa aac aaa cca aca ttg gat ttt gaa ctg ata aaa aca				1623
Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr				
	225	230	235	
gaa gcc aaa cag cct gcc acc cta agg aag tac tgt ata gag gca aag				1671
Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys				
	240	245	250	

cta acc aac aca aca aca gaa tct cgc tgc cca aca caa ggg gaa ccc	1719
Leu Thr Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro	
255 260 265 270	
agc cta aat gaa gag cag gac aaa agg ttc gtc tgc aaa cac tcc atg	1767
Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met	
275 280 285	
gta gac aga gga tgg gga aat gga tgt gga cta ttt gga aag gga ggc	1815
Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly	
290 295 300	
att gtg acc tgt gct atg ttc aga tgc aaa aag aac atg gaa gga aaa	1863
Ile Val Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys	
305 310 315	
gtt gtg caa cca gaa aac ttg gaa tac acc att gtg ata aca cct cac	1911
Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His	
320 325 330	
tca ggg gaa gag cat gca gtc gga aat gac aca gga aaa cat ggc aag	1959
Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys	
335 340 345 350	
gaa atc aaa ata aca cca cag agt tcc atc aca gaa gca gaa ttg aca	2007
Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr	
355 360 365	
ggc tat ggc act gtc aca atg gag tgc tct cca aga acg ggc ctc gac	2055
Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp	
370 375 380	
ttc aat gag atg gtg ttg ttg cag atg gaa aat aaa gct tgg ctg gtg	2103
Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val	
385 390 395	
cac agg caa tgg ttc cta gac ctg ccg tta cca tgg ttg ccc gga gcg	2151
His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala	
400 405 410	
gac aca caa ggg tca aat tgg ata cag aaa gag aca ttg gtc act ttc	2199
Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe	
415 420 425 430	
aaa aat ccc cat gcg aag aaa cag gat gtt gtt gtt tta gga tcc caa	2247
Lys Asn Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln	
435 440 445	
gaa ggg gcc atg cac aca gca ctt aca ggg gcc aca gaa atc caa atg	2295
Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met	
450 455 460	
tca tca gga aac tta ctc ttc aca gga cat ctc aag tgc agg ctg aga	2343
Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg	

465	470	475	
atg gac aag cta cag ctc aaa gga atg tca tac tct atg tgc aca gga Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly 480 485 490			2391
aag ttt aaa gtt gtg aag gaa ata gca gaa aca caa cat gga aca ata Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile 495 500 505 510			2439
gtt atc aga gtg caa tat gaa ggg gac ggc tct cca tgc aag atc cct Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro 515 520 525			2487
ttt gag ata atg gat ttg gaa aaa aga cat gtc tta ggt cgc ctg att Phe Glu Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile 530 535 540			2535
aca gtc aac cca att gtg aca gaa aaa gat agc cca gtc aac ata gaa Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu 545 550 555			2583
gca gaa cct cca ttc gga gac agc tac atc atc ata gga gta gag ccg Ala Glu Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro 560 565 570			2631
gga caa ctg aag ctc aac tgg ttt aag aaa gga agt tct atc ggc caa Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Ser Ile Gly Gln 575 580 585 590			2679
atg ttt gag aca aca atg agg ggg gcg aag aga atg gcc att tta ggt Met Phe Glu Thr Thr Met Arg Gly Ala Lys Arg Met Ala Ile Leu Gly 595 600 605			2727
gac aca gcc tgg gat ttt gga tcc ttg gga gga gtg ttt aca tct ata Asp Thr Ala Trp Asp Phe Gly Ser Leu Gly Gly Val Phe Thr Ser Ile 610 615 620			2775
gga aag gct ctc cac caa gtc ttt gga gca atc tat gga gct gcc ttc Gly Lys Ala Leu His Gln Val Phe Gly Ala Ile Tyr Gly Ala Ala Phe 625 630 635			2823
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tgg ata gga atg aat tca cgc agc acc tca ctg tct gtg aca cta gta Trp Ile Gly Met Asn Ser Arg Ser Thr Ser Leu Ser Val Thr Leu Val 655 660 665 670			2919
ttg gtg gga att gtg aca ctg tat ttg gga gtc atg gtg cag gcc Leu Val Gly Ile Val Thr Leu Tyr Leu Gly Val Met Val Gln Ala 675 680 685			2964
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<210> 43

<211> 685

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<400> 43

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Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg Asn Gly
 20             25             30
Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser Leu Leu
 35             40             45
Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala Met Asp
 50             55             60

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Leu	Gly	Glu	Leu	Cys	Glu	Asp	Thr	Ile	Thr	Tyr	Lys	Cys	Pro	Leu	Leu
65					70					75					80
Arg	Gln	Asn	Glu	Pro	Glu	Asp	Ile	Asp	Cys	Trp	Cys	Asn	Ser	Thr	Ser
				85					90					95	
Thr	Trp	Val	Thr	Tyr	Gly	Thr	Cys	Thr	Thr	Met	Gly	Glu	His	Arg	Arg
				100					105					110	
Glu	Lys	Arg	Ser	Val	Ala	Leu	Val	Pro	His	Val	Gly	Met	Gly	Leu	Glu
				115					120					125	
Thr	Arg	Thr	Glu	Thr	Trp	Met	Ser	Ser	Glu	Gly	Ala	Trp	Lys	His	Val
Gln	Arg	Ile	Glu	Thr	Trp	Ile	Leu	Arg	His	Pro	Gly	Phe	Thr	Met	Met
145															
Ala	Ala	Ile	Leu	Ala	Tyr	Thr	Ile	Gly	Thr	Thr	His	Phe	Gln	Arg	Ala
Leu	Ile	Phe	Ile	Leu	Leu	Thr	Ala	Val	Thr	Pro	Ser	Met	Thr	Met	Arg
Cys	Ile	Gly	Met	Ser	Asn	Arg	Asp	Phe	Val	Glu	Gly	Val	Ser	Gly	Gly
Ser	Trp	Val	Asp	Ile	Val	Leu	Glu	His	Gly	Ser	Cys	Val	Thr	Thr	Met
Ala	Lys	Asn	Lys	Pro	Thr	Leu	Asp	Phe	Glu	Leu	Ile	Lys	Thr	Glu	Ala
225															
Lys	Gln	Pro	Ala	Thr	Leu	Arg	Lys	Tyr	Cys	Ile	Glu	Ala	Lys	Leu	Thr
Asn	Thr	Thr	Thr	Glu	Ser	Arg	Cys	Pro	Thr	Gln	Gly	Glu	Pro	Ser	Leu
Asn	Glu	Glu	Gln	Asp	Lys	Arg	Phe	Val	Cys	Lys	His	Ser	Met	Val	Asp
Arg	Gly	Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly	Lys	Gly	Gly	Ile	Val
Thr	Cys	Ala	Met	Phe	Arg	Cys	Lys	Lys	Asn	Met	Glu	Gly	Lys	Val	Val
305															
Gln	Pro	Glu	Asn	Leu	Glu	Tyr	Thr	Ile	Val	Ile	Thr	Pro	His	Ser	Gly
Glu	Glu	His	Ala	Val	Gly	Asn	Asp	Thr	Gly	Lys	His	Gly	Lys	Glu	Ile
Lys	Ile	Thr	Pro	Gln	Ser	Ser	Ile	Thr	Glu	Ala	Glu	Leu	Thr	Gly	Tyr
Gly	Thr	Val	Thr	Met	Glu	Cys	Ser	Pro	Arg	Thr	Gly	Leu	Asp	Phe	Asn
Glu	Met	Val	Leu	Leu	Gln	Met	Glu	Asn	Lys	Ala	Trp	Leu	Val	His	Arg
385															
Gln	Trp	Phe	Leu	Asp	Leu	Pro	Leu	Pro	Trp	Leu	Pro	Gly	Ala	Asp	Thr
Gln	Gly	Ser	Asn	Trp	Ile	Gln	Lys	Glu	Thr	Leu	Val	Thr	Phe	Lys	Asn
Pro	His	Ala	Lys	Lys	Gln	Asp	Val	Val	Val	Leu	Gly	Ser	Gln	Glu	Gly
Ala	Met	His	Thr	Ala	Leu	Thr	Gly	Ala	Thr	Glu	Ile	Gln	Met	Ser	Ser
Gly	Asn	Leu	Leu	Phe	Thr	Gly	His	Leu	Lys	Cys	Arg	Leu	Arg	Met	Asp
465															
Lys	Leu	Gln	Leu	Lys	Gly	Met	Ser	Tyr	Ser	Met	Cys	Thr	Gly	Lys	Phe
Lys	Val	Val	Lys	Glu	Ile	Ala	Glu	Thr	Gln	His	Gly	Thr	Ile	Val	Ile
Arg	Val	Gln	Tyr	Glu	Gly	Asp	Gly	Ser	Pro	Cys	Lys	Ile	Pro	Phe	Glu

515	520	525
Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile Thr Val		
530	535	540
Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu Ala Glu		
545	550	555
Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro Gly Gln		
565	570	575
Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Ser Ile Gly Gln Met Phe		
580	585	590
Glu Thr Thr Met Arg Gly Ala Lys Arg Met Ala Ile Leu Gly Asp Thr		
595	600	605
Ala Trp Asp Phe Gly Ser Leu Gly Gly Val Phe Thr Ser Ile Gly Lys		
610	615	620
Ala Leu His Gln Val Phe Gly Ala Ile Tyr Gly Ala Ala Phe Ser Gly		
625	630	635
Val Ser Trp Thr Met Lys Ile Leu Ile Gly Val Ile Ile Thr Trp Ile		
645	650	655
Gly Met Asn Ser Arg Ser Thr Ser Leu Ser Val Thr Leu Val Leu Val		
660	665	670
Gly Ile Val Thr Leu Tyr Leu Gly Val Met Val Gln Ala		
675	680	685

<210> 44

<211> 5293

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> CDS

<222> (910)...(2964)

<400> 44

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ccgcatagtt	aagccagtat	ctgctccctg	cttgtgtgtt	ggaggtcgct	gagtagtgcg	120
cgagcaaaat	ttaagctaca	acaaggcaag	gcttgaccga	caattgcatg	aagaatctgc	180
ttaggggttag	gcggttttgcg	ctgcttcgcg	atgtacgggc	cagatatacg	cgttgacatt	240
gattattgac	tagttattaa	tagtaatcaa	ttacggggtc	attagttcat	agcccatata	300
tggagttccg	cgttacataa	cttacggtaa	atggcccggc	tggctgaccg	cccaacgacc	360
cccgccatt	gacgtcaata	atgacgtatg	ttcccatagt	aacgccaata	gggactttcc	420
attgacgtca	atgggtggag	tatttacggt	aaactgcca	cttggcagta	catcaagtgt	480
atcatatgcc	aagtacgccc	cctattgacg	tcaatgacgg	taaatggccc	gcctggcatt	540
atgccagta	catgacctta	tgggactttc	ctacttgcca	gtacatctac	gtattagtca	600
tcgctattac	catggtgatg	cggttttggc	agtacatcaa	tgggcgtgga	tagcggtttg	660
actcacgggg	atttccaagt	ctccacccca	ttgacgtcaa	tgggagtttg	ttttggcacc	720
aaaatcaacg	ggactttcca	aaatgtcgta	acaactccgc	cccattgacg	caaatgggcg	780
gtaggcgtgt	acggtgggag	gtctatataa	gcagagctct	ctggctaact	agagaaccca	840
ctgcttactg	gcttatcgaa	attaatacga	ctcactatag	ggagacccaa	gcttggtacc	900
gccgccgcc	atg ggc aag	agg tcc gcc	ggc tca atc	atg tgg ctc	gcg agc	951
	Met Gly Lys	Arg Ser Ala	Gly Ser Ile	Met Trp Leu	Ala Ser	
	1	5		10		

ttg gca gtt gtc	ata gct tgt	gca ggc gcc	ttc cat tta	acc aca	cgt	999
Leu Ala Val Val	Ile Ala Cys	Ala Gly Ala	Phe His Leu	Thr Thr	Arg	
15	20	25	30			

aac gga gaa cca cac atg atc gtc agc aga caa gag aaa ggg aaa agt Asn Gly Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser 35 40 45	1047
ctt ctg ttt aaa aca gag gat ggc gtg aac atg tgt acc ctc atg gcc Leu Leu Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala 50 55 60	1095
atg gac ctt ggt gaa ttg tgt gaa gac aca atc acg tac aag tgt ccc Met Asp Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro 65 70 75	1143
ctt ctc agg cag aat gag cca gaa gac ata gac tgt tgg tgc aac tct Leu Leu Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser 80 85 90	1191
acg tcc acg tgg gta act tat ggg acg tgt acc acc atg gga gaa cat Thr Ser Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His 95 100 105 110	1239
aga aga gaa aaa aga tca gtg gca ctc gtt cca cat gtg gga atg gga Arg Arg Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly 115 120 125	1287
ctg gag aca cga act gaa aca tgg atg tca tca gaa ggg gcc tgg aaa Leu Glu Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys 130 135 140	1335
cat gtc cag aga att gaa act tgg atc ttg aga cat cca ggc ttc acc His Val Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr 145 150 155	1383
atg atg gca gca atc ctg gca tac acc ata gga acg aca cat ttc caa Met Met Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln 160 165 170	1431
aga gcc ctg att ttc atc tta ctg aca gct gtc act cct tca atg aca Arg Ala Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr 175 180 185 190	1479
atg cgt tgc ata gga atg tca aat aga gac ttt gtg gaa ggg gtt tca Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser 195 200 205	1527
gga gga agc tgg gtt gac ata gtc tta gaa cat gga agc tgt gtg acg Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr 210 215 220	1575
acg atg gca aaa aac aaa cca aca ttg gat ttt gaa ctg ata aaa aca Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr 225 230 235	1623
gaa gcc aaa cag cct gcc acc cta agg aag tac tgt ata gag gca aag Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys 240 245 250	1671

cta acc aac aca aca aca gaa tct cgc tgc cca aca caa ggg gaa ccc	1719
Leu Thr Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro	
255 260 265 270	
agc cta aat gaa gag cag gac aaa agg ttc gtc tgc aaa cac tcc atg	1767
Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met	
275 280 285	
gta gac aga gga tgg gga aat gga tgt gga cta ttt gga aag gga ggc	1815
Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly	
290 295 300	
att gtg acc tgt gct atg ttc aga tgc aaa aag aac atg gaa gga aaa	1863
Ile Val Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys	
305 310 315	
gtt gtg caa cca gaa aac ttg gaa tac acc att gtg ata aca cct cac	1911
Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His	
320 325 330	
tca ggg gaa gag cat gca gtc gga aat gac aca gga aaa cat ggc aag	1959
Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys	
335 340 345 350	
gaa atc aaa ata aca cca cag agt tcc atc aca gaa gca gaa ttg aca	2007
Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr	
355 360 365	
ggt tat ggc act gtc aca atg gag tgc tct cca aga acg ggc ctc gac	2055
Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp	
370 375 380	
ttc aat gag atg gtg ttg ttg cag atg gaa aat aaa gct tgg ctg gtg	2103
Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val	
385 390 395	
cac agg caa tgg ttc cta gac ctg ccg tta cca tgg ttg ccc gga gcg	2151
His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala	
400 405 410	
gac aca caa ggg tca aat tgg ata cag aaa gag aca ttg gtc act ttc	2199
Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe	
415 420 425 430	
aaa aat ccc cat gcg aag aaa cag gat gtt gtt gtt tta gga tcc caa	2247
Lys Asn Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln	
435 440 445	
gaa ggg gcc atg cac aca gca ctt aca ggg gcc aca gaa atc caa atg	2295
Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met	
450 455 460	
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Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg	
465 470 475	
atg gac aag cta cag ctc aaa gga atg tca tac tct atg tgc aca gga	2391

Met	Asp	Lys	Leu	Gln	Leu	Lys	Gly	Met	Ser	Tyr	Ser	Met	Cys	Thr	Gly		
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aag	ttt	aaa	gtt	gtg	aag	gaa	ata	gca	gaa	aca	caa	cat	gga	aca	ata	2439	
Lys	Phe	Lys	Val	Val	Lys	Glu	Ile	Ala	Glu	Thr	Gln	His	Gly	Thr	Ile		
495					500					505					510		
ggt	atc	aga	gtg	caa	tat	gaa	ggg	gac	ggc	tct	cca	tgc	aag	atc	cct	2487	
Val	Ile	Arg	Val	Gln	Tyr	Glu	Gly	Asp	Gly	Ser	Pro	Cys	Lys	Ile	Pro		
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Phe	Glu	Ile	Met	Asp	Leu	Glu	Lys	Arg	His	Val	Leu	Gly	Arg	Leu	Ile		
			530					535					540				
aca	gtc	aac	cca	att	gtg	aca	gaa	aaa	gat	agc	cca	gtc	aac	ata	gaa	2583	
Thr	Val	Asn	Pro	Ile	Val	Thr	Glu	Lys	Asp	Ser	Pro	Val	Asn	Ile	Glu		
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Ala	Glu	Pro	Pro	Phe	Gly	Asp	Ser	His	Ile	Ile	Ile	Gly	Val	Glu	Pro		
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Gly	Gln	Leu	Lys	Leu	Asn	Trp	Phe	Lys	Lys	Gly	Ser	Ser	Ile	Gly	Gln		
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Met	Phe	Glu	Thr	Thr	Met	Arg	Gly	Ala	Lys	Arg	Met	Ala	Ile	Leu	Gly		
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Trp	Met	Gly	Val	Asn	Ala	Arg	Asp	Arg	Ser	Ile	Ala	Leu	Ala	Phe	Leu		
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<210> 45

<211> 685

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<400> 45

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Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser Leu Leu
      35             40             45
Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala Met Asp
      50             55             60
Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro Leu Leu
65             70             75             80
Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser Thr Ser
      85             90             95
Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His Arg Arg

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Glu	Lys	Arg	Ser	Val	Ala	Leu	Val	Pro	His	Val	Gly	Met	Gly	Leu	Glu	
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	130					135					140					
Gln	Arg	Ile	Glu	Thr	Trp	Ile	Leu	Arg	His	Pro	Gly	Phe	Thr	Met	Met	
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Ala	Ala	Ile	Leu	Ala	Tyr	Thr	Ile	Gly	Thr	Thr	His	Phe	Gln	Arg	Ala	
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Cys	Ile	Gly	Met	Ser	Asn	Arg	Asp	Phe	Val	Glu	Gly	Val	Ser	Gly	Gly	
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Ala	Lys	Asn	Lys	Pro	Thr	Leu	Asp	Phe	Glu	Leu	Ile	Lys	Thr	Glu	Ala	
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Lys	Gln	Pro	Ala	Thr	Leu	Arg	Lys	Tyr	Cys	Ile	Glu	Ala	Lys	Leu	Thr	
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Thr	Cys	Ala	Met	Phe	Arg	Cys	Lys	Lys	Asn	Met	Glu	Gly	Lys	Val	Val	
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Gln	Pro	Glu	Asn	Leu	Glu	Tyr	Thr	Ile	Val	Ile	Thr	Pro	His	Ser	Gly	
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Glu	Glu	His	Ala	Val	Gly	Asn	Asp	Thr	Gly	Lys	His	Gly	Lys	Glu	Ile	
			340					345					350			
Lys	Ile	Thr	Pro	Gln	Ser	Ser	Ile	Thr	Glu	Ala	Glu	Leu	Thr	Gly	Tyr	
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	370					375					380					
Glu	Met	Val	Leu	Leu	Gln	Met	Glu	Asn	Lys	Ala	Trp	Leu	Val	His	Arg	
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Gln	Trp	Phe	Leu	Asp	Leu	Pro	Leu	Pro	Trp	Leu	Pro	Gly	Ala	Asp	Thr	
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Gln	Gly	Ser	Asn	Trp	Ile	Gln	Lys	Glu	Thr	Leu	Val	Thr	Phe	Lys	Asn	
			420					425					430			
Pro	His	Ala	Lys	Lys	Gln	Asp	Val	Val	Val	Leu	Gly	Ser	Gln	Glu	Gly	
		435					440					445	</			

Pro Pro Phe Gly Asp Ser His Ile Ile Ile Gly Val Glu Pro Gly Gln
565 570 575
Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Ser Ile Gly Gln Met Phe
580 585 590
Glu Thr Thr Met Arg Gly Ala Lys Arg Met Ala Ile Leu Gly Asp Thr
595 600 605

Ala Trp Asp Phe Gly Ser Leu Gly Gly Val Phe Thr Ser Ile Gly Lys
610 615 620
Ala Leu His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly
625 630 635 640
Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met
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660 665 670
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<210> 46
<211> 5293
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<221> CDS
<222> (910)...(2964)

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cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180
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tggagttccg cgttacataa cttacggtaa atggcccggc tggctgaccg cccaacgacc 360
cccgccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 420
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gccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc 951
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser
1 5 10
ttg gca gtt gtc ata gct tgt gca ggc gcc ttc cat tta acc aca cgt 999
Leu Ala Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg
15 20 25 30

aac gga gaa cca cac atg atc gtc agc aga caa gag aaa ggg aaa agt 1047
Asn Gly Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser

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			50					55					60							
atg	gac	ctt	ggg	gaa	ttg	tgt	gaa	gac	aca	atc	acg	tac	aag	tgt	ccc	1143				
Met	Asp	Leu	Gly	Glu	Leu	Cys	Glu	Asp	Thr	Ile	Thr	Tyr	Lys	Cys	Pro					
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ctt	ctc	agg	cag	aat	gag	cca	gaa	gac	ata	gac	tgt	tgg	tgc	aac	tct	1191				
Leu	Leu	Arg	Gln	Asn	Glu	Pro	Glu	Asp	Ile	Asp	Cys	Trp	Cys	Asn	Ser					
	80					85					90									
acg	tcc	acg	tgg	gta	act	tat	ggg	acg	tgt	acc	acc	atg	gga	gaa	cat	1239				
Thr	Ser	Thr	Trp	Val	Thr	Tyr	Gly	Thr	Cys	Thr	Thr	Met	Gly	Glu	His					
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Arg	Arg	Glu	Lys	Arg	Ser	Val	Ala	Leu	Val	Pro	His	Val	Gly	Met	Gly					
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cat	gtc	cag	aga	att	gaa	act	tgg	atc	ttg	aga	cat	cca	ggc	ttc	acc	1383				
His	Val	Gln	Arg	Ile	Glu	Thr	Trp	Ile	Leu	Arg	His	Pro	Gly	Phe	Thr					
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		160				165					170									
aga	gcc	ctg	att	ttc	atc	tta	ctg	aca	gct	gtc	act	cct	tca	atg	aca	1479				
Arg	Ala	Leu	Ile	Phe	Ile	Leu	Leu	Thr	Ala	Val	Thr	Pro	Ser	Met	Thr					
	175				180				185						190					
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Met	Arg	Cys	Ile	Gly	Met	Ser	Asn	Arg	Asp	Phe	Val	Glu	Gly	Val	Ser					
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	240					245					250									
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Ile	Val	Thr	Cys	Ala	Met	Phe	Arg	Cys	Lys	Lys	Asn	Met	Glu	Gly	Lys	
		305					310					315				
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	320					325					330					
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Glu	Ile	Lys	Ile	Thr	Pro	Gln	Ser	Ser	Ile	Thr	Glu	Ala	Glu	Leu	Thr	
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			435					440					445			
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Ser	Ser	Gly	Asn	Leu	Leu	Phe	Thr	Gly	His	Leu	Lys	Cys	Arg	Leu	Arg	
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Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile	
495 500 505 510	
gtt atc aga gtg caa tat gaa ggg gac ggc tct cca tgc aag atc cct	2487
Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro	
515 520 525	
ttt gag ata atg gat ttg gaa aaa aga cat gtc tta ggt cgc ctg att	2535
Phe Glu Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile	
530 535 540	
aca gtc aac cca att gtg aca gaa aaa gat agc cca gtc aac ata gaa	2583
Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu	
545 550 555	
gca gaa cct cca ttc gga gac agc tac atc atc ata gga gta gag ccg	2631
Ala Glu Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro	
560 565 570	
gga caa ctg aag ctc aac tgg ttt aag aaa gga agc acg ctg ggc aag	2679
Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Thr Leu Gly Lys	
575 580 585 590	
gcc ttt tca aca act ttg aag gga gct caa aga ctg gca gcg ttg ggc	2727
Ala Phe Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly	
595 600 605	
gac aca gcc tgg gac ttt ggc tct att gga ggg gtc ttc aac tcc ata	2775
Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile	
610 615 620	
gga aaa gcc gtt cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt	2823
Gly Lys Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe	
625 630 635	
ggg gga atg tct tgg atc aca caa ggg cta atg ggt gcc cta ctg ctc	2871
Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu	
640 645 650	
tgg atg ggc gtc aac gca cga gac cga tca att gct ttg gcc ttc tta	2919
Trp Met Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu	
655 660 665 670	
gcc aca ggg ggt gtg ctc gtg ttc tta gcg acc aat gtg cat gct	2964
Ala Thr Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala	
675 680 685	
taattagttt gagcggccgc tcgagcatgc atctagaggg ccctattcta tagtgtcacc	3024
taaagtctag agctcgctga tcagcctcga ctgtgccttc tagttgccag ccattctgtt	3084
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aataagggcg	acacggaaat	gttgaatact	catactcttc	ctttttcaat	attattgaag	5184
catttatcag	ggttattgtc	tcatgagcgg	atacatattt	gaatgtattt	agaaaaataa	5244
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<210> 47

<211> 685

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<400> 47

Met	Gly	Lys	Arg	Ser	Ala	Gly	Ser	Ile	Met	Trp	Leu	Ala	Ser	Leu	Ala
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Val	Val	Ile	Ala	Cys	Ala	Gly	Ala	Phe	His	Leu	Thr	Thr	Arg	Asn	Gly
			20					25					30		
Glu	Pro	His	Met	Ile	Val	Ser	Arg	Gln	Glu	Lys	Gly	Lys	Ser	Leu	Leu
			35					40					45		
Phe	Lys	Thr	Glu	Asp	Gly	Val	Asn	Met	Cys	Thr	Leu	Met	Ala	Met	Asp
			50					55					60		
Leu	Gly	Glu	Leu	Cys	Glu	Asp	Thr	Ile	Thr	Tyr	Lys	Cys	Pro	Leu	Leu
65						70				75				80	

Arg	Gln	Asn	Glu	Pro	Glu	Asp	Ile	Asp	Cys	Trp	Cys	Asn	Ser	Thr	Ser
				85					90					95	
Thr	Trp	Val	Thr	Tyr	Gly	Thr	Cys	Thr	Thr	Met	Gly	Glu	His	Arg	Arg
				100					105					110	
Glu	Lys	Arg	Ser	Val	Ala	Leu	Val	Pro	His	Val	Gly	Met	Gly	Leu	Glu
				115					120					125	
Thr	Arg	Thr	Glu	Thr	Trp	Met	Ser	Ser	Glu	Gly	Ala	Trp	Lys	His	Val
						135						140			
Gln	Arg	Ile	Glu	Thr	Trp	Ile	Leu	Arg	His	Pro	Gly	Phe	Thr	Met	Met
145						150						155			160
Ala	Ala	Ile	Leu	Ala	Tyr	Thr	Ile	Gly	Thr	Thr	His	Phe	Gln	Arg	Ala
						165								175	
Leu	Ile	Phe	Ile	Leu	Leu	Thr	Ala	Val	Thr	Pro	Ser	Met	Thr	Met	Arg
						180								190	
Cys	Ile	Gly	Met	Ser	Asn	Arg	Asp	Phe	Val	Glu	Gly	Val	Ser	Gly	Gly
							200							205	
Ser	Trp	Val	Asp	Ile	Val	Leu	Glu	His	Gly	Ser	Cys	Val	Thr	Thr	Met
							215							220	
Ala	Lys	Asn	Lys	Pro	Thr	Leu	Asp	Phe	Glu	Leu	Ile	Lys	Thr	Glu	Ala
225						230						235			240
Lys	Gln	Pro	Ala	Thr	Leu	Arg	Lys	Tyr	Cys	Ile	Glu	Ala	Lys	Leu	Thr
						245								255	
Asn	Thr	Thr	Thr	Glu	Ser	Arg	Cys	Pro	Thr	Gln	Gly	Glu	Pro	Ser	Leu
						260								270	
Asn	Glu	Glu	Gln	Asp	Lys	Arg	Phe	Val	Cys	Lys	His	Ser	Met	Val	Asp
							280							285	
Arg	Gly	Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly	Lys	Gly	Gly	Ile	Val
							295							300	
Thr	Cys	Ala	Met	Phe	Arg	Cys	Lys	Lys	Asn	Met	Glu	Gly	Lys	Val	Val
305						310								320	
Gln	Pro	Glu	Asn	Leu	Glu	Tyr	Thr	Ile	Val	Ile	Thr	Pro	His	Ser	Gly
						325								335	
Glu	Glu	His	Ala	Val	Gly	Asn	Asp	Thr	Gly	Lys	His	Gly	Lys	Glu	Ile
						340								350	
Lys	Ile	Thr	Pro	Gln	Ser	Ser	Ile	Thr	Glu	Ala	Glu	Leu	Thr	Gly	Tyr
							360							365	
Gly	Thr	Val	Thr	Met	Glu	Cys	Ser	Pro	Arg	Thr	Gly	Leu	Asp	Phe	Asn
							375							380	
Glu	Met	Val	Leu	Leu	Gln	Met	Glu	Asn	Lys	Ala	Trp	Leu	Val	His	Arg
385						390								400	
Gln	Trp	Phe	Leu	Asp	Leu	Pro	Leu	Pro	Trp	Leu	Pro	Gly	Ala	Asp	Thr
						405								415	
Gln	Gly	Ser	Asn	Trp	Ile	Gln	Lys	Glu	Thr	Leu	Val	Thr	Phe	Lys	Asn
						420								430	
Pro	His	Ala	Lys	Lys	Gln	Asp	Val	Val	Val	Leu	Gly	Ser	Gln	Glu	Gly
							440							445	
Ala	Met	His	Thr	Ala	Leu	Thr	Gly	Ala	Thr	Glu	Ile	Gln	Met	Ser	Ser
							455							460	
Gly	Asn	Leu	Leu	Phe	Thr	Gly	His	Leu	Lys	Cys	Arg	Leu	Arg	Met	Asp
465						470								480	
Lys	Leu	Gln	Leu	Lys	Gly	Met	Ser	Tyr	Ser	Met	Cys	Thr	Gly	Lys	Phe
						485								495	
Lys	Val	Val	Lys	Glu	Ile	Ala	Glu	Thr	Gln	His	Gly	Thr	Ile	Val	Ile
							505							510	
Arg	Val	Gln	Tyr	Glu	Gly	Asp	Gly	Ser	Pro	Cys	Lys	Ile	Pro	Phe	Glu
							520							525	
Ile	Met	Asp	Leu	Glu	Lys	Arg	His	Val	Leu	Gly	Arg	Leu	Ile	Thr	Val

530		535		540											
Asn	Pro	Ile	Val	Thr	Glu	Lys	Asp	Ser	Pro	Val	Asn	Ile	Glu	Ala	Glu
545					550					555					560
Pro	Pro	Phe	Gly	Asp	Ser	Tyr	Ile	Ile	Ile	Gly	Val	Glu	Pro	Gly	Gln
				565						570					575
Leu	Lys	Leu	Asn	Trp	Phe	Lys	Lys	Gly	Ser	Thr	Leu	Gly	Lys	Ala	Phe
			580					585					590		
Ser	Thr	Thr	Leu	Lys	Gly	Ala	Gln	Arg	Leu	Ala	Ala	Leu	Gly	Asp	Thr
			595				600						605		
Ala	Trp	Asp	Phe	Gly	Ser	Ile	Gly	Gly	Val	Phe	Asn	Ser	Ile	Gly	Lys
			610				615						620		
Ala	Val	His	Gln	Val	Phe	Gly	Gly	Ala	Phe	Arg	Thr	Leu	Phe	Gly	Gly
625							630								640
Met	Ser	Trp	Ile	Thr	Gln	Gly	Leu	Met	Gly	Ala	Leu	Leu	Leu	Trp	Met
				645					650						655
Gly	Val	Asn	Ala	Arg	Asp	Arg	Ser	Ile	Ala	Leu	Ala	Phe	Leu	Ala	Thr
			660				665								670
Gly	Gly	Val	Leu	Val	Phe	Leu	Ala	Thr	Asn	Val	His	Ala			
			675				680								685

<210> 48
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note =
 synthetic construct

<400> 48
 tgtgcaggcg ccttccattt aaccacacgt aacg

34

<210> 49
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note =
 synthetic construct

<400> 49
 tcgagcggcc gctcaactaa ttaggcctgc accatgactc

40

<210> 50
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note =
 synthetic construct

<400> 50
 cttatcgaaa ttaatacgac tcactatagg

30

<210> 51

<211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note =
 synthetic construct

 <400> 51
 atagattgct ccaaacactt ggtgg 25

 <210> 52
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note =
 synthetic construct

 <400> 52
 actccatagg aaaagccggt cacc 24

 <210> 53
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note =
 synthetic construct

 <400> 53
 gcgagctcta gcatttaggt gacactatag 30

 <210> 54
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note =
 synthetic construct

 <400> 54
 ctccaccaag tgtttggtgg tgccttcaga aca 33

 <210> 55
 <211> 11
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note =
 synthetic construct

 <400> 55

Leu His Gln Val Phe Gly Gly Ala Phe Arg Thr
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<210> 56

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
 synthetic construct

<400> 56

cttatcgaaa ttaatacgac tcactatagg

30

<210> 57

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
 synthetic construct

<400> 57

gaattcgtct cacttccttt cttaaaccag ttgagcttc

39

<210> 58

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
 synthetic construct

<400> 58

ggaattcgtc tcggaagcac gctgggcaag g

31

<210> 59

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
 synthetic construct

<400> 59

gcgagctcta gcatttaggt gacactatag

30

<210> 60

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<400> 60
aactggttta agaaaggaag cacgctgggc gcc

33

<210> 61
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<400> 61
Asn Trp Lys Lys Gly Ser Thr Leu Gly Lys Ala
1 5 10